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Use of yeasts with dsRNA virus-like particles for investigating the transcriptome-level effects of antivirals

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ABSTRACT

Use of yeasts with dsRNA virus-like particles for investigating the transcriptome-level effects of antivirals

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The emergence and re-emergence of virus-associated infectious diseases have significant influence on human health and society, and their control depends on both the efficiency and safety of antiviral drugs. There are around 90 chemicals have been formally licensed and prescribed for the treatment of viral infections. However, side effects of many antiviral drugs are largely unknown. Previous studies have focused on the effects of antiviral drugs on different viruses. While to understand the effects of antiviral drugs and to find their potential side effects, more studies should target on virus hosts, not only on viruses themselves. To fill in this research gap, this thesis aimed to characterize the effects of antiviral drugs (ribavirin and nitazoxanide) on virus host using *Saccharomyces cerevisiae* as a model

organism due to its many advantages such as its complete genome is available and it shares many common genes and biological processes with human. The specific aims include: 1) to test the effectiveness of ribavirin and nitazoxanide on *S. cerevisiae* killer strain, a strain which can kill other sensitive strains (Chapter II); 2) to characterize the effects of ribavirin on whole transcriptomes of *S. cerevisiae* strains containing dsRNA virus-like particles (Chapter III); and 3) to characterize effects of nitazoxanide on whole transcriptomes of *S. cerevisiae* strains containing dsRNA virus-like particles and *S. cerevisiae* cured strain (Chapter IV). The knowledge is scarce about the effects of ribavirin and nitazoxanide on eukaryotic organisms especially at their whole genome levels. This RNA-Seq-based study provides insights into how ribavirin and nitazoxanide impact on eukaryotic transcriptomes.

In Chapter I, background information of this thesis is presented. Particularly, a brief review of antivirals explained the necessity of more studies needed to clarify the safety and potential related mechanisms of the drugs. Literature survey of the two antiviral drugs used in this study (ribavirin and nitazoxanide) found that the related research areas are very active. Especially it was found that until now, there is no study utilizing RNA-Seq techniques to study the effects of ribavirin or nitazoxanide on the transcriptomes of the virus host. The powerful sequencing technique of RNA-Seq was utilized in this study as the main technique to detect the effects of antiviral drugs.

In Chapter II, the effectiveness of ribavirin and nitazoxanide on *S. cerevisiae* killer strain was tested. Two antivirals were used to cure the killer

strain respectively, and the curing results were confirmed by halo assay and gel electrophoresis experiment. Moreover, to eliminate the possibility of contamination, interdelta PCR was also conducted. Results showed that both ribavirin and nitazoxanide were effective to cure the *S. cerevisiae* killer strain. Actually M dsRNA virus-like particles were removed from the killer strain and the killer strain also lost its killing character, indicating that the killer toxin was encoded in M dsRNA. Results of interdelta PCR also excluded the possibility of contamination. This chapter developed new methods to cure the killer strain of *S. cerevisiae* and provided a solid foundation for the following chapters, which aimed at characterizing the effects of the antiviral drugs utilizing *S. cerevisiae* as a model organism.

In Chapter III, based on the results of Chapter II, effects of ribavirin on whole transcriptomes of *S. cerevisiae* strains containing dsRNA virus-like particles were characterized by RNA-Seq. Three different strains, including S288C, S7 and MS300c were tested in this study. Ribavirin exposure experiment was conducted at two different time points, including 1 h and 4 h with the concentration of 100 μM of ribavirin for three different strains. Total RNA was extracted from samples exposed to ribavirin and the respective negative controls and proceeded to RNA sequencing. After RNA-Seq data analysis, I found small nuclear (sn)RNAs and small nucleolar (sno)RNAs in *S. cerevisiae* exposed to ribavirin were accumulated first and then reduced. Each snRNA or snoRNA molecule assembles with protein molecules to form a snRNP or a snoRNP, respectively. While small RNPs, including snRNPs and snoRNPs, are known to be associated with human diseases such as spinal muscular atrophy, dyskeratosis congenital, and

Prader-Willi syndrome (Matera et. al. , 2007). Thus, there may be a need to scrutinize the relationships between side effects and small RNPs in patients who are treated with ribavirin.

In Chapter IV, based on the successful results and insightful hints obtained from Chapter III, another important potential broad-spectrum antiviral drug nitazoxanide was chose to study. Nitazoxanide is in clinical test for antiviral utilization and the potential side effects have not be known yet. Thus RNA-Seq was used to characterize effects of nitazoxanide on whole transcriptomes of *S. cerevisiae* strains containing dsRNA virus-like particles. Strains of S288C, S7, MS300c and cured strain obtained from Chapter II were tested. Nitazoxanide exposure experiment was conducted at two time-points 1 h and 4 h with the concentration of 10 μg/ml of nitazoxanide for four strains. RNA-Seq experiment condition was similar to Chapter III. Compared to the negative controls of each library, differentially expressed genes, enrichment GO terms and over (under)-representation of KEGG pathways were detected. Results showed that ribosome biogenesis function was largely influenced and ribosome assembly factors were significantly differentially expressed in *S. cerevisiae* strains exposed to nitazoxanide. Ribosome dysfunctions are known to be related with several important diseases such as male infertility, neurological defects and so on. This chapter provides insightful hints to the potential side effects of nitazoxanide and it might be significant since the drug is in clinical test now for reaching the antiviral medicine market.

In summary, this thesis utilized the powerful sequencing technique, RNA-Seq, to characterize the effects of antivirals on *S. cerevisiae* at the whole

transcriptome level. This study is significant when considering ribavirin's and nitazoxanide's potential side effects related to dysregulation of small non-coding RNAs and ribosome biogenesis in humans who are treated for the viral infections by them, which is of great value for pharmaceutical and medical industry. In addition, it provided insights for ecological risk assessment that the similar defects may happen on other eukaryotes in the environment when antiviral drugs are released to the surroundings. Besides, this study developed the new and efficient method to screen important antiviral drugs to seek for their potential side effects and underlying reasons in the future.

Keywords: *S. cerevisiae*, ribavirin, nitazoxanide, antivirals, side effect, mycovirus, RNA-Seq

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LIST OF ABBREVIATIONS

ANE: Alopecia, Neurological defects, and Endocrinopathy

CT: Cycle Threshold

DE: Differentially Expressed

dsRNA: Double-Stranded RNA

ER: Endoplasmic Reticulum

FPKM: Fragments Per Kilobase Million

GO: Gene Ontology

HBV: Hepatitis B Virus

HCV: Hepatitis C Virus

HIV: Human Immunodeficiency Virus

KEGG: Kyoto Encyclopedia of Genes and Genomes

LSU: Large Subunit

MBA: Methylene Blue Agar

mRNA-Seq: mRNA Sequencing

mtRNAs: mitochondrial RNAs

NAIC: Native American Indian Childhood Cirrhosis

ncRNAs: non-coding RNAs

NF1: Neurofibromatosis Type 1

NGS: Next-Generation Sequencing

NTZ: Nitazoxanide

OMIM: Online Mendelian Inheritance in Man

PE: Paired End

Peg-IFN: Pegylated Interferon

POAG: Primary Open Angle Glaucoma

qPCR: Quantitative Polymerase Chain Reaction

qRT-PCR: Quantitative Reverse Transcription Polymerase Chain Reaction

RNA-Seq: RNA Sequencing

rRNA: Ribosomal RNA

RSV: Respiratory Syncytial Virus

RT-PCR: Reverse Transcription Polymerase Chain Reaction

S. cerevisiae: *Saccharomyces cerevisiae*

SGD: Saccharomyces Genome Database

snoRNAs: small nucleolar RNAs

snoRNPs: small nucleolar ribonucleoproteins

snRNAs: small nuclear RNAs

snRNPs: small nuclear ribonucleoproteins

SRS: Silver-Russell Syndrome

SSU: Small Subunit

WTSS: Whole Transcriptome Shotgun Sequencing

YPD: Yeast Peptone Dextrose

CHAPTER I.

BACKGROUNDS

Antivirals

Over the past two decades, there has been a growing interest in the increasing number of viruses that cause unexpected illness and epidemics among humans, wildlife and livestock. The well-known important virus-related diseases include human immunodeficiency virus (HIV) infections (Barre-Sinoussi et. al. , 2013), hepatitis B virus (HBV) infections (Rehermann and Nascimbeni, 2005), hepatitis C virus (HCV) infections (Rehermann and Nascimbeni, 2005), influenza virus infections (Petrova and Russell, 2018) and so on. For instance, from 2011 to 2017, globally there is a total of 1,307 virus associated diseases epidemic events in 172 countries according to "Managing epidemics" by WHO in 2018, causing fear and panic across the world, and inflicting enormous economic damage. Correspondingly, the demand for antivirals has increased markedly. Until 2016, 90 chemicals have been formally approved for the treatment of viral infections, almost half of which are intended to treat HIV infections(De Clercq, 2004, De Clercq and Li, 2016, Littler and Oberg, 2005). And these approved antiviral drugs could be arbitrarily divided into 13 functional groups such as nucleoside analogues, nucleotide reverse transcriptase inhibitors, protease inhibitors and so on (De Clercq and Li, 2016). At the same time, the safety of utilizing antivirals to treat human with the specific infections should also been noticed. Side effects of several antiviral drugs have been reported such as the dermatological adverse events during ribavirin treatment of people with HCV infections (Teuber et. al. , 2001, Fontana, 2009, Cacoub et. al. , 2012). Moreover, the interferon therapy for

HBV disease was confirmed to cause severe side effects including all of the symptoms of a classic influenza virus infection and has been shown to be associated with increased levels of suicide (Brenard, 1997). Thus, more studies are needed to develop new antiviral drugs and at the same time, the safety of antiviral drugs expected to reach the market and the existing antiviral drugs should be clarified.

Among these antiviral drugs, Ribavirin, 1-β-D-ribofuranosyl-1H-1, 2, 4-triazole-3-carboxamide, is an antiviral medication effective against three RNA viruses: HCV, RSV (Respiratory Syncytial Virus), and influenza virus, and mainly used to treat HCV infections (De Clercq and Li, 2016, Bougie and Bisaillon, 2004, Sidwell et. al. , 1972). The molecular structure is shown in Figure 1-1 (A). It was first synthesized in 1970 by researchers at ICN pharmaceuticals (now Valent International Pharmaceuticals) (Thomas et. al. , 2012). Ribavirin is a guanosine analog that can inhibit viral syntheses, but the mechanisms of treatment are not fully understood. Nonetheless, several mechanisms of action have been proposed (Patterson and Fernandez-Larsson, 1990), including depletion of intracellular pools of guanosine triphosphate by a guanosine analog ribavirin (Smee and Matthews, 1986, Smee et. al. , 2001, Streeter et. al. , 1973). Lethal mutagenesis of viral RNA is another proposed mechanism (Ortega-Prieto et. al. , 2013, Dietz et. al. , 2013, Crotty et. al. , 2002, Bull et. al. , 2005). Additionally, ribavirin is thought to inhibit viral RNA-dependent RNA polymerases (Eriksson et. al. , 1977, Maag et. al. , 2001) and synthesis of a guanine pyrophosphate structure at the 5’ cap of viral mRNA (Goswami et. al. , 1979). Side effects have been also reported in HCV patients treated with ribavirin in

combination with pegylated interferon (Peg-IFN), with reported symptoms including hematologic, dermatologic, and neuropsychiatric disorders (Sulkowski et. al. , 2011). Until now, there are many studies done for ribavirin. Table 1-1 showed the number of literature related to ribavirin found by SCOPUS as of November 2018. There are totally 30336 literatures related to the word "ribavirin", more than 40% of which are related to HCV treatment researches (Table 1-1). There are also considerable amount of literatures focusing on ribavirin and influenza (1800), and ribavirin and HBV (907). Regarding the side effects and mechanism of ribavirin, researchers are also making great efforts to find them out. Therefore, the ribavirin related studies are still necessary and very active.

Another potential broad-spectrum antiviral drug, Nitazoxanide (NTZ), 2-acetyloxy-*N*-(5-nitro-2-thiazolyl) benzamide , is a broad-spectrum anti-infective drug that markedly modulates the survival, growth, and proliferation of a range of extracellular and intracellular protozoa, helminths, anaerobic bacteria (Fox and Saravolatz, 2005). The molecular structure of nitazoxanide is shown in Figure 1-1 (B). Initially, nitazoxanide was developed as a treatment of intestinal protozoan infections. Its antiviral properties against HBV and HCV were coincidentally discovered when the drug was being evaluated to treat cryptosporidiosis in HIV patients coinfected with HBV or HCV(Rossignol and Keeffe, 2008). Since then, nitazoxanide has been shown to inhibit the replication of HBV, HCV (Korba et. al. , 2008), Japanese encephalitis virus (Shi et. al. , 2014), rubella virus (Perelygina et. al. , 2017) and influenza virus(Rossignol et. al. , 2009) in cells. Until November of 2018, there are 1658 studies about nitazoxanide

found by SCOPUS (Table 1-2). Among these, 239 literatures were related to antiviral studies, since it is a newly discovered potential broad-spectrum antiviral drug. There are also 232 and 231 literatures regarding the mechanism and side effect, respectively of nitazoxanide (Table 1-2). In a summary, there is still much room for improvement and discovering in the research area related to nitazoxanide.

Besides, antiviral drugs have been recently recognized as one of the emerging contaminants in the environment. They have gained attention due to the fact that they escape the degradation step in wastewater treatment plants (WWTPs) and finished into surface and groundwater sources (Prasse et. al. , 2010). Furthermore, direct effects such as acute toxicity and indirect effects such as impacts on the reproduction ability have been pointed out. However, except for oseltamivir and its active metabolite oseltamivir carboxylate, the potential human, animal and ecological risks associated with the discharge of the antiviral drugs to the environment are not well documented due to their "unknown effects"(Jain et. al. , 2013).

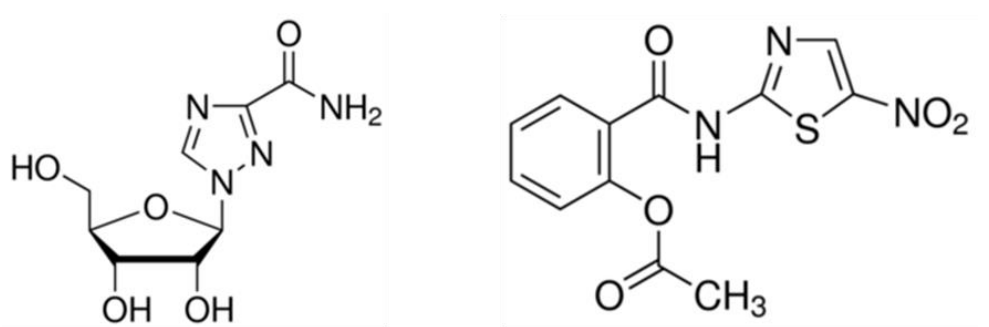


Figure 1-1. Molecular structure of ribavirin and nitazoxanide. (A) Ribavirin; (B) Nitazoxanide

Table 1-1. Number of literature related to ribavirin found by SCOPUS as of November 2018.

Search words	Number of literature
Ribavirin	30336
RNA-Seq	15990
Ribavirin + HCV	12603
Ribavirin + Influenza	1800
Ribavirin + HBV	907
Ribavirin + side effect	5102
Ribavirin + mechanism	2943
Ribavirin + *Saccharomyces cerevisiae*	12
Ribavirin + RNA-Seq	3
Ribavirin + human + RNA-Seq	3
Ribavirin + *Saccharomyces cerevisiae* + RNA-Seq	1

Table 1-2. Number of literature related to nitazoxanide found by SCOPUS as of November 2108.

Search words	Number of literature
Nitazoxanide	1658
Nitazoxanide + Influenza	74
Nitazoxanide + antiviral	239
Nitazoxanide + side effect	231
Nitazoxanide + mechanism	232
Nitazoxanide + *Sacchromyces cerevisiae*	0
Nitazoxanide + RNA-Seq	0
Nitazoxanide + Human + RNA-Seq	0
Nitazoxanide + *Saccharomyces cerevisiae* + RNA-Seq	0

Saccharomyces cerevisiae

To study the effects of antivirals on the virus hosts, a model organism should be carefully chosen and utilized. As the researchers pointed out that such organisms should have certain advantages, for example: “a) they may help overcome ethical and experimental constraints that hold for the target life form, b) they provide a framework on which to develop and optimize

analytical methods that facilitate and standardize analysis, and c) they are thought to be representative of a larger class of living beings for whatever biological phenomenon or process the community is interested in" (Karathia et. al. , 2011). *Saccharomyces cerevisiae* (*S. cerevisiae*) is a good choice based on these criteria. *S. cerevisiae* is a species of yeast. The name *Saccharomyces cerevisiae* is composed of two parts: The first part "Saccharomyces" means "sugar fungus" in Latinized Greek, while the second part "cerevisiae" is derived from Latin and has the meaning "of beer". *S. cerevisiae* is the most important eukaryotic cellular model system. It is the first eukaryotic organism whose complete DNA sequence was released and it is a fine model organism for interpreting and understanding human DNA sequences (Botstein et. al., 1997). *S. cerevisiae* is known as one of the useful yeasts which are utilized in baking, brewing and other industries (Moyad, 2008), whose strains specialized for fermentation have been extensively studied (Fay and Benavides, 2005, Mortimer and Polsinelli, 1999). Saccharomyces Genome Database (SGD) provides comprehensive integrated biological information for the yeast *S. cerevisiae* along with search and analysis tools to explore these data, enabling the discovery of functional relationships between sequence and gene products in fungi and higher organisms (Cherry et. al. , 2012). *S. cerevisiae* shares many genes and many basic biological properties with human cells, but grow a lot faster (Botstein et. al. , 1997). So it's easy and cheap to use *S. cerevisiae* as a model organism to test drugs compared to similar experiments in more complex animals such as mice and zebrafish. It has already been used as a model to study aging (Murakami and Kaeberlein, 2009), regulation of gene

expression (Biddick and Young, 2009), signal transduction (Hohmann et. al. , 2007), cell cycle (Nasheuer et. al. , 2002), metabolism (Brocard-Masson and Dumas, 2006, Lopez-Mirabal and Winther, 2008), apoptosis (Owsianowski et. al. , 2008), neurodegenerative disorders (Miller-Fleming et. al. , 2008), and many other biological processes. Researchers have found that more than 31% of all the potential protein-coding genes of yeast have homolog among mammalian protein sequences, many human disease related genes (out of 2271 known disease-associated genes, 526 genes) have been reported to have a close orthologues in the yeast genome, which represents the value of yeast as a model system (Forslund et. al. , 2011). These facts explain the significant role of yeast as a model organism for human disorders. Thus, *S. cerevisiae* was chosen as a model organism to study the effects of antivirals in this research.

Mycovirus

Mycovirus or fungal viruses are viruses that specifically infect fungi and the majority of them have double-stranded RNA (dsRNA) genomes. Some strains of *S. cerevisiae* host dsRNA virus-like particles that encode toxic proteins of K1, K2, or K28 (Schmitt and Tipper, 1990, Schmitt and Breinig, 2006, Wickner, 1986). More recently, a new *S. cerevisiae* killer toxin (Klus), encoded by a double-stranded RNA (dsRNA) virus was isolated (Rodriguez-Cousino et. al. , 2011). These toxins are lethal to the susceptible strains of the same or related yeast species and spoil processes of fermentation (Young and Yagiu, 1978). However, they are immune to their own toxin or to toxins produced by strains of the same killer type (Magliani

et. al. , 1997, Schmitt and Breinig, 2006). K1, K2, K28 and Klus killer toxins are genetically encoded by medium-size dsRNA viruses grouped into four types, M1, M2, M28, and ScV-Mlus of 1.6, 1.5, 1.8, and 2.1 kb, respectively (Young and Yagiu, 1978, Schmitt and Tipper, 1990, Rodriguez-Cousino et. al., 2011). The toxin-coding M viruses depend on a second large (4.6-kb) dsRNA helper virus, L-A(BC), for maintenance and replication (Wickner, 1996). This study aimed to use mycovirus to simulate disease-associated virus, and use the yeast as a model for eukaryotic organisms to evaluate the effects of antiviral drugs on virus host. To reach this, a powerful technique is needed which can reach the molecular level to seek for the potential reasons and underlying mechanisms of associated effects. Thus, RNA-Seq was utilized in this study.

RNA Sequencing (RNA-Seq)

Recently, RNA Sequencing was used for fungal transcriptome analyses (Nookaew et. al. , 2012, Wang et. al., 2009). RNA sequencing (RNA-Seq), also called whole transcriptome shotgun sequencing (WTSS), a technique based on deep sequencing technologies to count the numbers of transcripts at the whole genome level in a biological sample at a given moment (Wang et. al. , 2009, Anders and Huber, 2010). The typical RNA-Seq experiment process and data analysis techniques have been discussed by many researchers. Briefly, long RNAs are first converted into a library of cDNA fragments. Sequencing adaptors are subsequently added to each cDNA fragment and a short sequence is obtained from each cDNA using high-throughput sequencing technology. The resulting sequence reads are filtered

by quality and aligned with the reference genome or transcriptome (Wang et. al., 2009, Xu and Yamamoto, 2017).

Whole transcriptome analysis is useful when characterizing the genome-wide gene expressions of fungi exposed to anti-viral drugs, and can provide important information about the mechanisms underlying drug treatment (DeFilippis et. al. , 2003). Traditionally, DNA microarrays are used to analyze the whole transcriptomes of fungi in response to different experimental factors (DeFilippis et. al., 2003). As shown in Table 1-3, compared to microarray method, RNA-Seq works well for investigating both known transcripts and exploring new ones. And RNA-Seq delivers low background signal. Additionally, RNA-Seq has the ability to quantify a large dynamic range of expression levels and accurate when quantifying genes expressed at low or high levels (Wang et. al., 2009). The results of RNA-Seq are comparable to those obtained by using quantitative PCR. As shown in Table 1-1, there are 15990 literatures regarding RNA-Seq, while only 3 literatures related to the search word "ribavirin + RNA-Seq". The paper matched the search word "ribavirin + *Saccharomyces cerevisiae* + RNA-Seq" is our paper, studying the effects of ribavirin on yeast *S. cerevisiae* (Xu and Yamamoto, 2017), published in 2017 (Chapter III). It indicates that our study (Chapter III) was the frontier research, which utilized *S. cerevisiae* as a model organism to study the effects of ribavirin on the whole transcriptome level by RNA-Seq. According to Table 1-2, there are no published literatures related to nitazoxanide and RNA-Seq or matching the searching word "Nitazoxanide + *Saccharomyces cerevisiae*". Therefore, as far as I know, our study will be the first study utilizing RNA-

Seq techniques to study the effects of nitazoxanide on the whole transcriptomes of the yeast *S. cerevisiae*.

Objectives

This study aims to characterize effects of antivirals (ribavirin and nitazoxanide) on human model species *S. cerevisiae* strains containing dsRNA virus-like particles through studying its whole transcriptomes using RNA-Seq. The specific goals include: 1) Effectiveness of ribavirin and nitazoxanide on *S. cerevisiae* killer strain will be tested; 2) to characterize effects of ribavirin on human model *S. cerevisiae* strains containing dsRNA virus-like particles through studying transcriptomes of using RNA-Seq; 3) to characterize effects of nitazoxanide on human model *S. cerevisiae* strains containing dsRNA virus-like particles and *S. cerevisiae* cured strains, through studying transcriptomes of using RNA-Seq.

Table 1-3. Advantages of RNA-Seq compared with other transcriptomic methods (Wang et. al., 2009).

Technology	Tiling microarray	cDNA or EST sequencing	RNA-Seq
Technology specifications			
Principle	Hybridization	Sanger sequencing	High-throughput sequencing
Resolution	From several to 100 bp	Single base	Single base
Throughput	High	Low	High
Reliance on genomic sequence	Yes	No	In some cases
Background noise	High	Low	Low
Application			
Simultaneously map transcribed regions and gene expression	Yes	Limited for gene expression	Yes
Dynamic range to quantify gene expression level	Up to a few-hundredfold	Not practical	>8,000-fold
Ability to distinguish different isoforms	Limited	Yes	Yes
Ability to distinguish allelic expression	Limited	Yes	Yes
Practical issues			
Required amount of RNA	High	High	Low
Cost for mapping transcriptomes of large genomes	High	High	Relatively low

CHAPTER II.

Effectiveness of ribavirin and nitazoxanide on

S. cerevisiae killer strain

Introduction

The killer strains of *S. cerevisiae* hold the abilities to kill sensitive strains by secreting a killer toxin and immunity to the action of the killer toxin (Wickner, 1974). Killer (K), sensitive (S), and neutral (N) phenotypes of *S. cerevisiae* were first described by Makower and Bevan (Bevan EA, 1963). As shown in Table 2-1, the *S. cerevisiae* killer strains of the types K1, K2, K28 and Klus possess two double-stranded RNA plasmids, which are enclosed on a protein capsid. The larger dsRNA is called L-plasmid and the smaller one M-plasmid (Wickner, 1993, Wickner, 1996). The presence of a satellite M dsRNA in cells coinfected with an L-A dsRNA is responsible for the production of killer toxin (Schmitt and Tipper, 1995). Toxins K1 and K2 are very similar in their mode of action, both of which cause plasma membrane damage (Marquina et. al. , 2002). While the K28 killer toxin differs from K1 and K2 toxins in that it can inhibit nuclear DNA synthesis (Schmitt et. al. , 1996).

These toxins are lethal to the susceptible strains and spoil processes of fermentation (Young and Yagiu, 1978). It has been reported that killer strains of the type K1 and K2 of *Saccharomyces cerevisiae* (*S. cerevisiae*) that are known to harbor dsRNA-virus like particles were cured successfully by heat treatment or eukaryote protein synthesis inhibitor cycloheximide (Pieczynska et. al. , 2013, Fink and Styles, 1972). However, heat treatment is not effective to cure the K28 killer strain of *S. cerevisiae* (J. Zorg, 1988).Thus more effective approaches are needed.

Table 2-1. Types of *S. cerevisiae* dsRNA viruses.

Virus	Virus function	dsRNA (kb)	Encoded proteins
ScV-L-A (B or C)	Helper virus, responsible for virus replication	4.6	Gag-major capsid protein required for virus particle assembly, Pol-RNA dependent RNA polymerase required for virus genome replication
ScV-M1	Killer virus, exists as a satellite of helper virus	1.6	K1 preprotoxin – major precursor for mature secreted toxin, also required for self-immunity to K1
ScV-M2	Killer virus, exists as a satellite of helper virus	1.5	K2 preprotoxin – major precursor for mature secreted toxin, also required for self-immunity to K2
ScV-M28	Killer virus, exists as a satellite of helper virus	1.8	K28 preprotoxin – major precursor for mature secreted toxin, also required for self-immunity to K28
ScV-Mlus	Killer virus, exists as a satellite of helper virus	2.1-2.3	Klus preprotoxin – major precursor for mature secreted toxin, also required for self-immunity to Klus

Ribavirin is a kind of antiviral drug, which is widely used for HCV, HBV, and influenza infections treatment (De Clercq and Li, 2016). Nitazoxanide is a newly discovered antiviral drug which potentially has a broad-spectrum antiviral ability (Rossignol and Keeffe, 2008). Ribavirin is likely effective to remove dsRNA particles from the yeast *S. cerevisiae* as studies demonstrated it removed dsRNA elements from filamentous fungi (Herrero and Zabalgogeazcoa, 2011, Jiang et. al. , 2015, Park et. al. , 2006, Rodríguez-García et. al. , 2014, Rodriguez-Cousino et. al., 2011). Curing ability of nitazoxanide is still subject to be studied. However, it has been reported that nitazoxanide is effective to inhibit the replication of rotavirus, which is a genus of double-stranded RNA virus (Rossignol, 2014). This indicates that nitazoxanide may be also effective to remove the dsRNA virus in the yeast *S. cerevisiae*. But the underlying removal or inactivation mechanisms are still not known.

Until now, the killing system related research problems existing in *S. cerevisiae* strains are not fully understood. More studies are still necessary to fill in the blank and to add more supplementary information about the killing mechanism, interaction with the environment and so on. Furthermore, *S. cerevisiae* strains will be used as the model organisms to characterize the effects of antiviral drugs ribavirin and nitazoxanide. To be an appropriate and better model system in this study, information should be developed about if the two antiviral drugs were effective on the *S. cerevisiae* contained virus. Only after confirming the two antiviral drugs are effective, *S. cerevisiae* can be used to simulate the “virus hosts”. Therefore, this chapter aimed to study the effectiveness of these two antiviral drugs on *S. cerevisiae* killer strain. This chapter will provide supplementary information to the yeast virulence study and also provide background information for the following two chapters,

which aimed at characterizing the effects of the antiviral drugs utilizing *S. cerevisiae* as a model organism.

Materials and Method

Curing of killer strain

Curing experiments of strain MS300c were carried out by growing the yeast in 10 ml yeast peptone dextrose (YPD) (Becton, Dickinson and Company, Sparks, MD, USA) broth in the presence of nitazoxanide (100 µg/ml) (CAS 55981-09-4; Sigma-Aldrich, St. Louis, MO, USA)(Broekhuysen et. al. , 2000) or ribavirin (100 µM) (CAS 36791-04-5; Sigma-Aldrich, St. Louis, MO, USA) (Herrero and Zabalgogeazcoa, 2011, Jiang et. al., 2015, Parker, 2005) for 3 days. After broth culture, the yeast suspension was spread on YPD agar. Single colonies were randomly picked and subsequently analyzed for halo assay and loss of the toxin-coding M dsRNA by agarose gel electrophoresis.

Verification of the curing assay

Halo assay of the isolated colonies and MS300c strain against the S288C strain as lawn strain was done on methylene blue agar (MBA) plates. The agar was adjusted at pH 4.7 with citrate-phosphate buffer. The assay was conducted at 20 ºC for 6 days (Carroll et. al. , 2009). The colonies without killing zone were chosen to check for the loss of M dsRNA. RNA was extracted from 100-200 mg (wet weight) of each chosen colony. Samples were frozen in liquid nitrogen and ground to fine powders for RNA extraction following the protocol recommended by Double-RNA viral dsRNA extraction mini kit (ABC Scientific, Glendale, CA, USA). Briefly, appropriate amount of cells were ground, vigorously vortexed before adding chloroform. After centrifuge, supernatant was transferred and washed twice. The entire sample mixture was washed twice after utilizing binding buffer.

The extracted RNA was analyzed by electrophoresis on 1% (w/v) agarose gels and stained by SYBR Gold nucleic acid gel stain (Invitrogen, cat. no. S11494). Results were obtained through the G:Box Chemi-XL1.4 Gel imaging system (Syngene, Cambridge, UK). The colonies losing the M dsRNA were used for interdelta PCR.

Table 2-2. *S. cerevisiae* strains used in this study.

Strain name	Relevant genotypes or features	Description	Reference
ATCC 204508 (S288C)	MATα *SUC2 mal mel gal2 CUP1 flo1 flo8-1 hap1*	L-A/L-BC virus-like particle	(Wickner, 1983)
ATCC 44828 (S7)	MATα *DET1-1* [L-A-HN L-(BC)	L-A dsRNA virus-like particle	(Oliver et. al. , 1977, Wickner, 1983)
ATCC 201204 (MS300c)	MATa *leu2 ura3-52 ski2-2* [L-A L-BC (L-28) M-28]	L-A and M28 dsRNA virus-like particles	(Schmitt et. al., 1996)
MS300c-	Not available	L-A dsRNA virus-like particle	This study

Interdelta PCR

Individual strains of *S. cerevisiae* can be distinguished based on specific DNA regions, known as inter-delta regions, flanked by Ty-elements (Legras and Karst, 2003). Therefore, inter-delta PCR can be used to distinguish different strains of *S. cerevisiae*. To confirm the cured strains were truly originated from MS300c killer strain and excluding the possibility of potential contamination, interdelta PCR typing was carried out to distinguish different *S. cerevisiae* strains. The conditions for interdelta PCR typing by δ 1 (5'-CAAAATTCACCTATATTCTCA-3') and δ 2 (5'-GTGGATTTTTATTCCAACA-3') were as follows: initial denaturation cycle at 94 ℃for 4 min, followed by 30 cycles of amplification-denaturation at 94 ℃ for 30 s, annealing at 49 ℃ for 1 min and extension at 72 ℃ for 2 min. The final extension was at 72 ℃ for 10 min (Suranska et. al. , 2016). PCR products were separated and detected on 1.5% (w/v) agarose gel at 5 V cm^{-1} for 3-4 h. The gels were stained by SYBR Gold nucleic acid gel stain and visualized by the G:Box Chemi-XL1.4 Gel imaging system.

Results

Curing of killer strain

Curing of killer strain experiments were conducted with the presence of ribavirin and nitazoxanide respectively. To test the curing result of ribavirin and nitazoxanide, both cured colonies and original killer colonies (as control) were place onto the MBA plates on which lawn of sensitive strains had been spread (halo assay). The appearance of killing zone can be seen in 5-6 days

of incubation at 20 ℃. As shown in Figure 2-1, the killer colonies were surrounded by a clear killing zone on MBA plates. A clear zone with a deep blue color indicated death of the sensitive cells, while there is no killing zone around cured colonies. This indicates the cured strains lost their killer trait by utilizing ribavirin and nitazoxanide. According to the halo assay results, both ribavirin and nitazoxanide were able to remove the killer trait of *S. cerevisiae* killer strain.

To determine the genetic backgrounds of the cured colonies, RNA was also extracted from the colonies without killing zone and the colonies with killing zone, and proceeded to the gel electrophoresis experiment. As shown in the gel image Figure 2-2, the cured strains have lost the M-dsRNA, while for the killer strain, both M-dsRNA and L-dsRNA were detected.

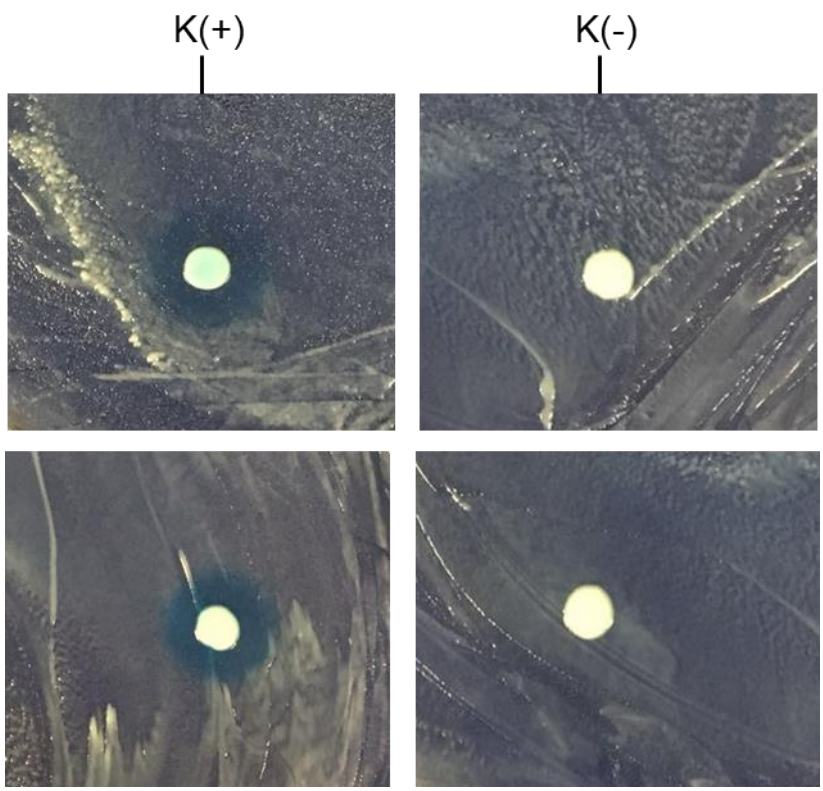


Figure 2-1. Killer toxin assay of the MS300c strain against the S288C strain as lawn strains. The methylene blue agar was adjusted at pH 4.7 with citrate-phosphate buffer. The assay was conducted at 20 ºC for 6 days. K (+): original killer strain MS300c showing killing zone; K (-): cured strain by ribavirin or nitazoxanide, showing no killing effect.

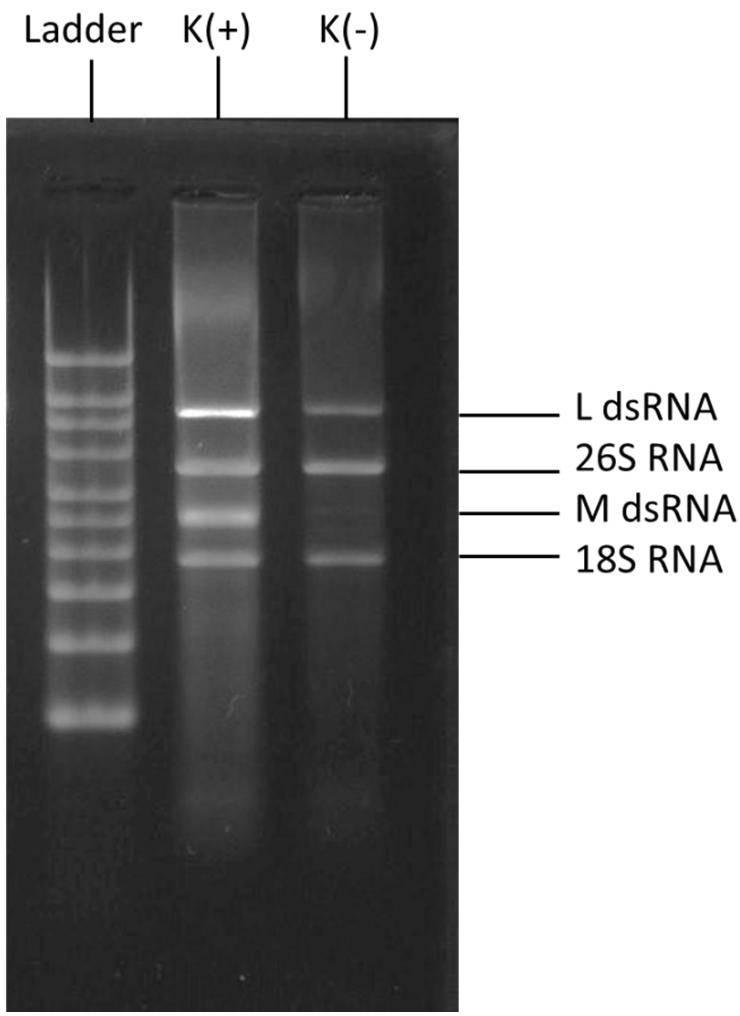


Figure 2-2. Gel electrophoresis results of extracted RNA from MS300c strain and cured strain. K (+): MS300c killer strain with both L and M dsRNA bands; K (-) cured strain with only L dsRNA.

Results of interdelta PCR

To confirm the cured strains were truly originated from MS300c killer strain and eliminate the possibility of potential contamination, interdelta PCR typing was carried out to distinguish different *S. cerevisiae* strains. *S. cerevisiae* strains of S288C, S7 were used as controls. As shown in Figure 2-3, compared with two controls, cured strain has the same pattern with the original MS300c killer strain, different with that of controls, indicating that the cured strain was truly originated from MS300c killer strain.

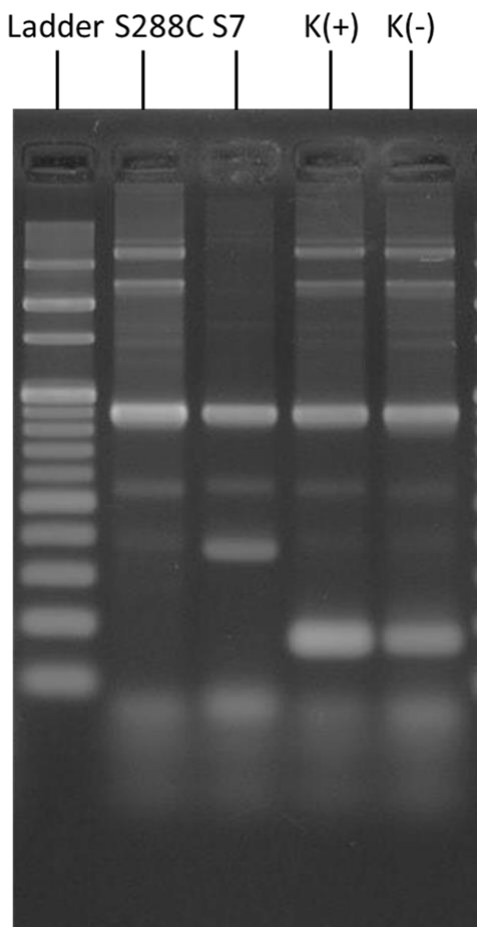


Figure 2-3. Gel electrophoresis results of interdelta PCR typing. S288C:

S288C strain of *S. cerevisiae*, used as control; S7: S7 strain of *S. cerevisiae*, used as control; K(+): MS300c killer strain; K(-): cured strain from MS300c killer strain.

Discussion

This study utilized antiviral drugs, ribavirin and nitazoxanide, to cure the killer strain MS300c of *S. cerevisiae* and successfully converted the killer strain into a sensitive non-killer strain. Cured strains lost M dsRNA and killer character. Our studies showed that the killer strain MS300c of *S. cerevisiae* has the ability to kill other sensitive strains that it has a clear killing zone shown in the halo assay test (Figure 2-1). This phenomenon was difficult to be observed previously because the killing occurs only with media of low pH and not on standard petri plates (Fink and Styles, 1972).

The ribavirin concentration used in this study was 100 μM, the pharmacologically relevant concentration (10-100 μM) (Zimmerman and Deeprose, 1978, Smee and Matthews, 1986, Rankin et. al. , 1989, Jiang et. al., 2015, Parker, 2005). The nitazoxanide exposure concentration we chose, 10 μg/ml, was described as the peak concentration of the drug in human plasma after receiving a single 500-mg oral dose of nitazoxanide (Broekhuysen et. al., 2000). These exposure concentrations can provide insights into how ribavirin and nitazoxanide impact on eukaryotic transcriptomes, which is thought to be important when determining elusive mechanisms of action and potential side effects of the two antiviral drugs on human. On the other hand, the cytotoxic concentration of ribavirin on chick primary fibroblast cell line was 25 μg/ml (Azeem et. al. , 2015), higher than

the exposure concentration used in our study 100 μM (about 24 μg/ml). And another study showed that ribavirin inhibited cell proliferation for different cells (human hepatocellular carcinoma cells and Chinese hamster ovary cells) at different concentration but was absent of cytotoxic effects (Librelotto et. al. , 2017). The nitazoxanide cytotoxicity was less than 5% if cells (human umbilical vein endothelial cells) were treated with less than 10 μg/ml for uninfected cells (Ludmila Perelygina, 2017). And some other researchers also pointed out that the 50% cytotoxic concentration of NIZ on cells (monkey kidney MA104 cells and human colorectal adenocarcinoma Caco-2 and HT-29 cells) was higher than 50 μg/ml (La Frazia et. al. , 2013). Our study showed that the antiviral drug, ribavirin and nitazoxanide, both are effective to remove the M dsRNA from *S. cerevisiae* killer strain (Figure 2-2). Several other researchers reported curing the killer strains of *S. cerevisiae* by high temperature or cycloheximide, a kind of protein synthesis inhibitor. For instance, it was reported that cycloheximide causes a dramatic increase in conversion of several killer strains of *S. cerevisiae* to sensitive, non-killer strains (Fink and Styles, 1972). Another research group found K1 and K2 type killer strain of *S. cerevisiae* can be cured by high temperature (up to 40 ℃) (J. Zorg, 1988). Our study added some new methods to cure the *S. cerevisiae* killer strain. Compared to previous curing methods, including high incubation temperature and protein synthesis inhibitor cycloheximide, are indirectly methods to affect viral dsRNA replication, the method developed in this chapter is new in terms of functional way and potential underlying mechanism. Although the mechanism of curing is unknown, Fink and Styles (Fink and Styles, 1972) pointed out the potential

mechanism for cycloheximide was that cytoplasmic ribosomal protein synthesis must be necessary for the replication of the genetic determinant since cycloheximide inhibits eukaryotic protein synthesis. This action could limit the genetic determinant and may cause it to be diluted as cell division progress. Further studies are needed to figure out the mechanisms underlying the curing fact. Our study also confirmed that the cured strains lost the M dsRNA while the L dsRNA was left, which is consistent with other literatures (J. Zorg, 1988, Schmitt and Tipper, 1992). More studies are needed to figure out this phenomenon and underlying mechanisms.

To the best of our knowledge, the present study is the first study utilizing antiviral ribavirin and nitazoxanide to successfully cure the K28 type killer strain of *S. cerevisiae*. Indeed, the dsRNA viruses in the strain MS300c were seems to be stable in our hands: they were difficult to be cured by cycloheximide or high temperature, same thing that other researchers also met before (Pieczynska et. al., 2013).

This study developed new approaches of the conversion of killer *S. cerevisiae* strain to non-killer, sensitive strain, which will be important for yeast virulence study and also as the supplementary interpretation of the action mechanisms of ribavirin and nitazoxanide. Also, these results demonstrated ribavirin and nitazoxanide were effective to act on *S. cerevisiae* strain, which is a good preliminary background for the following two chapters, which aim to study the effects of these two antivirals on yeast *S. cerevisiae*.

CHAPTER III.

Characterization of effects of ribavirin on whole transcriptomes of *S. cerevisiae* strains containing dsRNA virus-like particles by RNA-Seq.

(This chapter has been published under the title "mRNA-Seq reveals accumulation followed by reduction of small nuclear and nucleolar RNAs in yeast exposed to antiviral ribavirin" in *FEMS Yeast Research*, Volume 17, Issue 7, fox 067, 2017)

Introduction

S. cerevisiae is a yeast species widely studied as a model organism for gene functions and interactions (Tong et. al. , 2004, Costanzo et. al. , 2010), metabolism (Lopez-Mirabal and Winther, 2008), and viral infections (Wickner et. al. , 2013). Some strains host dsRNA virus-like particles that encode toxic proteins of K1, K2, or K28 (Wickner, 1986, Schmitt and Tipper, 1990, Schmitt and Breinig, 2006). Cycloheximide is used to cure viral infections in yeast (Fink and Styles, 1972). Similarly, ribavirin is likely effective as studies demonstrated it removed dsRNA elements from filamentous fungi (Herrero and Zabalgogeazcoa, 2011, Rodríguez-García et. al., 2014, Jiang et. al., 2015, Park et. al., 2006).

Ribavirin is an antiviral drug that is effective for a wide range of human viruses such as respiratory syncytial virus, Lassa virus, and HCV (Bougie and Bisaillon, 2004, Sidwell et. al., 1972). Ribavirin is a guanosine analog that can inhibit viral syntheses, but the mechanisms of action are not fully understood. Several mechanisms of action have been proposed (Patterson and Fernandez-Larsson, 1990), which include depletion of intracellular pools of guanosine triphosphate by a guanosine analog ribavirin (Streeter et. al., 1973, Smee and Matthews, 1986, Smee et. al., 2001). Lethal mutagenesis of viral RNA is another proposed mechanism (Bull et. al., 2005, Crotty et. al., 2002, Dietz et. al., 2013, Ortega-Prieto et. al., 2013). Additionally, ribavirin is thought to inhibit viral RNA-dependent RNA polymerases (Eriksson et. al., 1977, Maag et. al., 2001) and synthesis of a guanine pyrophosphate structure at the 5’ cap of viral mRNA (Goswami et.

al., 1979). Side effects have also been reported in HCV patients treated with ribavirin in combination with pegylated interferon (Peg-IFN), with reported symptoms including hematologic, dermatologic, and neuropsychiatric disorders (Sulkowski et. al., 2011).

However, the side effects of ribavirin utilization are still largely unknown, which is an emerging serious problem in medical treatments. Furthermore, the effects of releasing the antiviral drug ribavirin to the environment are still unknown, which is also a gap for the environmental risk assessment studies. Thus, more studies are needed to characterize the effects of ribavirin on virus hosts. The knowledge is scarce about effects of ribavirin on eukaryotic organisms especially at their whole genome levels. Therefore this RNA-Seq-based study aims at characterizing the effects of ribavirin on *S. cerevisiae*, which is used as a model organism in this study.

Materials and Methods

Preparation of the tested strains

Three *S. cerevisiae* strains of ATCC 44828 (S7) (MATα *DET1-1* [L-A-HN L-(BC)]) (Wickner, 1983, Oliver et. al., 1977), ATCC 201204 (MS300c) (MATa *leu2 ura3-52 ski2-2* [L-A L-BC (L-28) M-28]) (Schmitt et. al., 1996), and ATCC 204508 (S288C) (MATα *SUC2 mal mel gal2 CUP1 flo1 flo8-1 hap1*) (Sherman, 2002)were tested. Three strains were cultured on the yeast peptone dextrose (YPD) (Becton, Dickinson and Company, Sparks, MD, USA) agar plates at 30°C for 48 h, and a single colony of each strain was picked and suspended in 10 ml saline (0.85%) with Tween 20 (1%). The concentrations of yeast in the suspensions were determined by plating

the suspensions on YPD agar plates and enumerating the cultured colonies after 2-day incubation at 30°C. The suspensions were inoculated in 4.5 ml of YPD broth with the initial concentration adjusted at 2.5×10^5 CFU ml^{-1}. The viable concentration might be reduced from 2.5×10^5 CFU ml^{-1} during 2-day storage of the suspensions (at room temperature) to enumerate cultured colonies, but the optimal recovery of RNA (50–100 mg) could be achieved from yeasts cultured in the broths adjusted with this initial concentration. It should also be stated that reductions in the yeast viabilities did not affect our transcriptome analyses since the same suspension, despite a reduction in the viability, was used for each pair of the sample exposed to ribavirin and the respective negative control. The inocula were incubated at 30°C by gently shaking using an orbital shaker (SLRM-3, Seoul in Bioscience, Seoul, Korea) for 16 h.

Ribavirin exposures

After 16 h of the incubation, 0.5 ml solution of 1 mM ribavirin (Sigma-Aldrich, St. Louis, MO, USA) in 1% DMSO (Sigma-Aldrich) was added to each of the 4.5 ml cultured suspensions. The resultant final concentrations were 100 μM for ribavirin (Herrero and Zabalgogeazcoa, 2011, Jiang et. al., 2015, Parker, 2005) and 0.1% for DMSO. Only 0.5 ml solution of 1% DMSO was added to negative controls. The samples of three strains were incubated at 30°C with agitation for 1 h or 4 h after the addition of ribavirin in 1% DMSO or 1% DMSO only. The samples were harvested by centrifugation at 10,000 g for 10 min, weighed, and snap-frozen in liquid

nitrogen for RNA extraction. Biological triplicates were taken on three different days for each strain.

RNA extraction and sequencing

Total RNA was extracted from 50–100 mg (wet weight) of each sample from three strains. About 1 μg of total RNA from each sample was used to enrich poly (A)-containing RNA by the TruSeq mRNA Sample Prep kit v2 (Illumina, Inc., San Diego, CA, USA). The resultant RNA was primed with random hexamers to synthesize first strand cDNA. Double-stranded cDNA was synthesized and purified by the Agencourt AMPure XP kit (Beckman Coulter, Inc., Pasadena, CA, USA). Index adapters were attached to the cDNA, enriched, and quantitated by qPCR and the LabChip GX HT DNA High Sensitivity Kit (PerkinElmer, Waltham, MA, USA). Indexed libraries were treated with the HiSeq PE (Paired-End) Cluster Kit v3 cBot and the TruSeq SBS v3-HS kit (Illumina). Paired-end (2 × 100 bp) sequencing was performed by Illumina HiSeq 2000. Raw sequences were uploaded to the BioProject database of the NCBI under accession number SRP080972.

Sequence data processing and analyses

Both forward and reverse reads after removing the adapter and low quality sequences were mapped against the reference genome of *S. cerevisiae* S288C (GCF_000146045.2) by using the Tophat version 2 with default parameters (Trapnell et. al. , 2009).The fragments per kilobase of exon per million reads mapped (FPKM) values were calculated, and differentially expressed (DE) genes were determined by the pooled model (Anders and Huber, 2010) of the Cuffdiff in Cufflinks package version 2.1.1 (Trapnell et.

al. , 2010). DE genes were based on biological triplicates of each ribavirin exposed sample relative to biological triplicates of respective negative controls exposed to 0.1% DMSO only. The DE genes were defined when uncorrected *p*-value was greater than the FDR adjusted *p*-value (*q*-value) after Benjamin-Hochberg correction for multiple-testing. The full and slimmed gene ontology (GO) terms were determined for the DE gene sets for each sample by the Cytoscape (Shannon et. al. , 2003) plugin the BiNGO version 3.0.3 (Maere et. al. , 2005) against the GO annotation file for *S. cerevisiae* S288C genome, i.e., gene_association.sgd, submitted on June 25, 2016 to the Gene Ontology Consortium (Ashburner et. al., 2000, Gene Ontology, 2015) The up- and down-regulated genes were analyzed separately (Hong et. al. , 2014). The hypergeometric test was used. Variant callings in transcripts were examined as a measure of point mutations that might be caused by incorporation of ribavirin molecules. The quality trimmed sequences were mapped against the reference genome of *S. cerevisiae* S288C by using the Burrows-Wheeler Alignment tool version 1.2.3 with default parameters (Li and Durbin, 2009). Variant callings in the mapped transcripts of *snR34*, *snR35*, and *snR37* of the S288C strain exposed to ribavirin for 1 h were examined. These genes were selected since they showed distinct time-course tendency of accumulation followed by reduction. The numbers of total nucleotides and variant callings in the transcripts were counted by visualizing variant callings by the Integrative Genomic Viewer version 2.3 (Robinson et. al. , 2011, Thorvaldsdottir et. al. , 2013).

Results

Sequencing statistics and summary

For each library, 8,504,320 to 14,278,183 sequences were mapped to the reference genome of *S. cerevisiae* S288C, representing 69- to 115-fold coverages of redundancy according to the equation given by Lander and Waterman (1988) (Table 3-1). A total of 5,934 transcribed genes were detected, representing 93% of the 6,350 known genes of the *S. cerevisiae* S288C strain. The mean FPKM values of the biological triplicates of each transcribed gene for each sample are shown in Figure 3-1a. A total of 109 DE genes were detected (Table 3-A1), with the number ranging from 2 to 60 for the up-regulated genes and from 4 to 27 for the down-regulated genes for samples exposed to ribavirin relative to basal transcript levels in the respective negative controls exposed to 0.1% DMSO only (Figure 3-1b). Venn diagram (Figure 3-1c) showed the common up- and down-regulated genes between each strain.

Table 3-1. Number and coverage of cDNA sequences in the three *S. cerevisiae* strains.

Strain	Type	Time (h)	Replicate	Total reads [a]	Mapped reads [b]	Fraction of mapped reads (%)	Coverage [c]
ATCC 204508 (S288C)	Control	1	1	15220058	14110693	92.7	114.1
			2	15159130	14135711	93.2	114.3
			3	15563554	14278183	91.7	115.4
		4	1	13035816	12111149	92.9	97.9
			2	13829607	12811704	92.6	103.6
			3	15244210	14137767	92.7	114.3
	Exposed	1	1	13072412	12118380	92.7	98.0
			2	14505988	13612477	93.8	110.0
			3	12859095	11886440	92.4	96.1
		4	1	14228793	13276999	93.3	107.3
			2	15153845	13902336	91.7	112.4
			3	13593274	12562100	92.4	101.5
ATCC 44828 (S7)	Control	1	1	15576428	14182280	91.0	114.6
			2	12097262	11117312	91.9	89.9
			3	12546265	11497457	91.6	92.9
		4	1	11209631	10285600	91.8	83.1
			2	11873752	10824356	91.2	87.5
			3	11382220	10444550	91.8	84.4
	Exposed	1	1	10994556	9999558	91.0	80.8
			2	12183170	11120536	91.3	89.9
			3	11242360	10339355	92.0	83.6
		4	1	10201949	9336365	91.5	75.5
			2	11911948	10884732	91.4	88.0

			3	10131222	9260995	91.4	74.9
ATCC 201204 (MS300c)	Control	1	1	12232684	9622362	78.7	77.8
			2	12013169	9262878	77.1	74.9
			3	16587748	13452649	81.1	108.8
		4	1	11767658	9372998	79.7	75.8
			2	14045127	10605196	75.5	85.7
			3	16102653	13084405	81.3	105.8
	Exposed	1	1	11600804	9283596	80.0	75.0
			2	12621174	9862507	78.1	79.7
			3	15558939	12431738	79.9	100.5
		4	1	10937564	8504320	77.8	68.7
			2	13703666	10731551	78.3	86.7
			3	15374074	11787769	76.7	95.3

a The number of the pairs of forward and reverse sequence reads after quality trimming.

b The number of the pairs of forward and reverse sequence reads mapped to the reference genome of S288C by the Tophat2.

c The coverages were estimated by the equation given by Lander and Waterman (1988) and derived by dividing the number of total read bases by the average haploid genome size of *S. cerevisiae* S288C (24.991364 Mb).

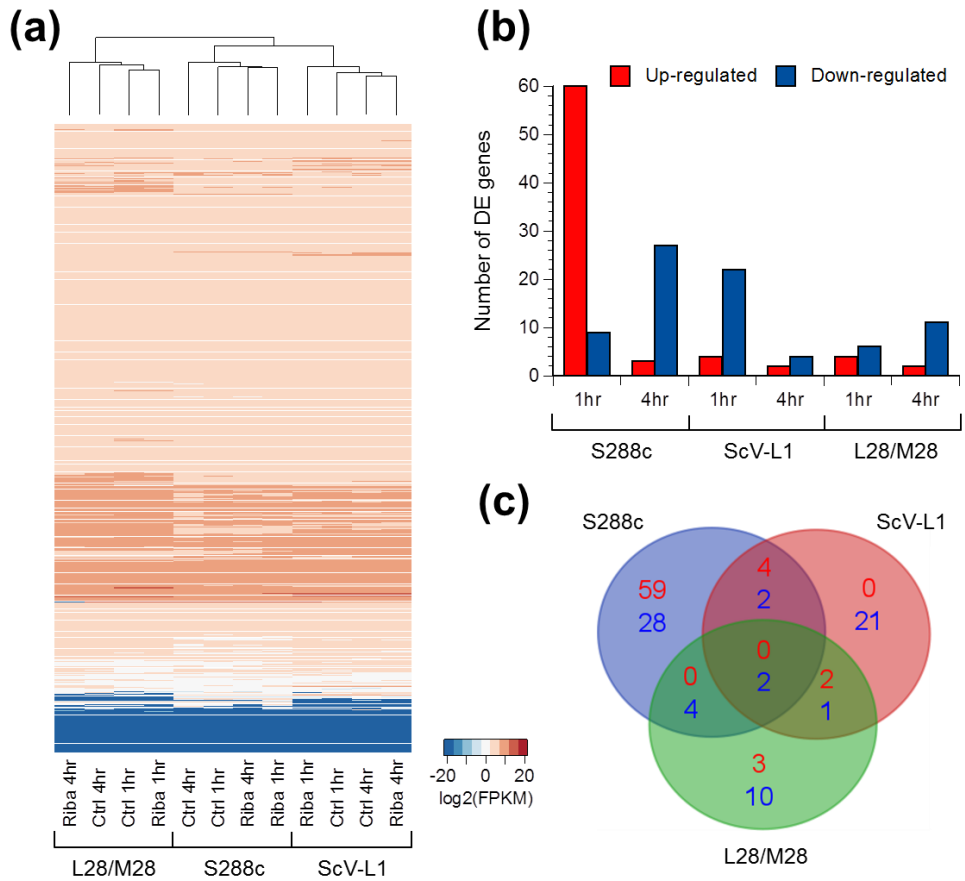


Figure 3-1. (a) Global transcriptomes of the ATCC 204508 (S288C), ATCC 44828 (ScV-L1), and ATCC 201204 (L28/M28) *S. cerevisiae* strains. The Euclidean distances are shown based on log-transformed FPKM values of all 5,934 transcribed genes. (b) Number of DE genes relative to the respective controls exposed to 0.1% DMSO only. (c) Venn diagrams illustrating overlaps of DE genes across each strain and exposure time. Numbers in red and blue indicate up- and down-regulated genes, respectively, that are combined for the two time points of 1 h and 4 h.

GO terms

The significantly over-represented GO terms were determined based on the up-regulated and down-regulated gene sets for each strain at each time point. The slimmed GO terms are shown in Figure 3-2. No slimmed GO term was found for the gene sets down-regulated at 1 h and up-regulated at 4 h in the S288C and MS300c strains. The five most significant slimmed GO terms were RNA modification guide activity (GO: 0030555), rRNA binding (GO: 0019843), nucleolus (GO: 0005730), RNA modification (GO: 0009451), and rRNA processing (GO: 0006364) for the gene sets up-regulated at 1 h and down-regulated at 4 h in the S288C and S7 strains, and for the gene set down-regulated at 4 h in the MS300c strain (Figure 3-2). For the S288C strain, 97 out of 159 GO terms based on the gene set down-regulated at 4 h were found also in the GO terms based on the gene set up-regulated at 1 h (Figure 3-2). The similar tendency was found for the S7 strain (Figure 3-2). The full GO terms are listed in Tables 3-A2 to 3-A10. No full GO term was found for the gene sets down-regulated at 1 h and up-regulated at 4 h in the S288C strain, and for the gene set up-regulated at 4 h in the MS300c strain.

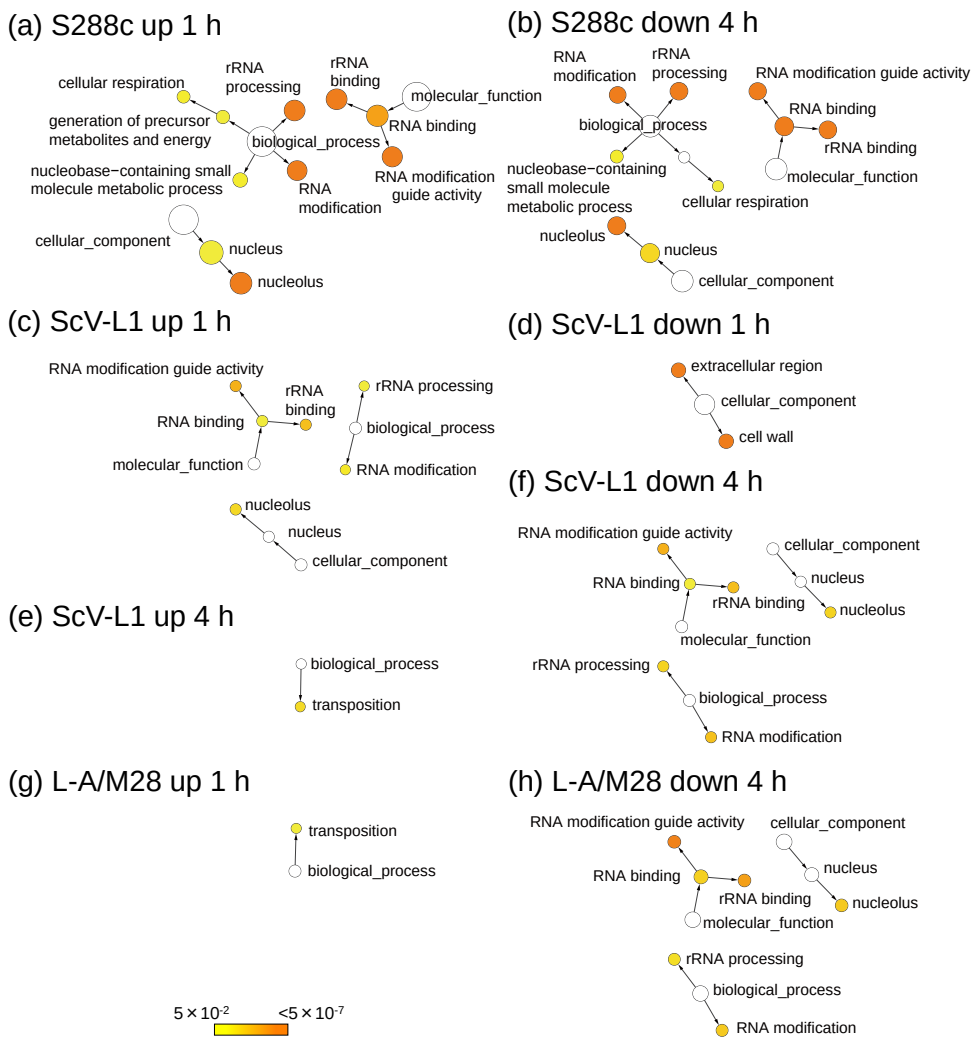


Figure 3-2. Slimmed GO terms based on the DE gene sets (a) up-regulated at 1 h in the S288C strain, (b) down-regulated at 4 h in the S288C strain, (c) up-regulated at 1 h in the ScV-L1 strain, (d) down-regulated at 1 h in the ScV-L1 strain, (e) up-regulated at 4 h in the ScV-L1 strain, (f) down-regulated at 4 h in the ScV-L1 strain, (g) up-regulated at 1 h in the L-A/M28 strain, and (h) down-regulated at 4 h in the L-A/M28 strain. The size of each node is proportional to the expected number of genes in each GO term. The connection between each node represents hierarchy of GO terms. Yellow to

orange colors indicate nodes with statistical significance (*p*-values). Nodes in white are not significantly overrepresented. No slimmed GO term was found for the samples that are not shown in this figure.

DE genes

Figure 3-3 shows fold changes of transcript levels of the DE genes found in the significantly over-represented full GO terms in which more than 3 DE genes were detected. The tendencies of the DE genes shown in Figure 3-3 are thought to be robust since the reproducibility of transcriptional tendencies of each gene was ensured within a gene by triplicate experiments as well as across the genes in the same functional category. A total of 31 *snR* genes, including *LSR1* also known as *snR20*, were differentially detected in at least one of the three tested strains at 1 and/or 4 h (Table 3-S2). Most of the significant *snR* genes were up-regulated at 1 h, but down-regulated at 4 h. In the S288C strain, 27 *snR* genes were significantly up-regulated at 1 h, and 18 *snR* genes, including *LSR1*, were significantly down-regulated at 4 h. The similar but less distinct tendency was observed in the S7 and MS300c strains. In the S7 strain, 3 *snR* genes (*snR35*, *snR37*, and *snR190*) were significantly up-regulated at 1 h, and 3 *snR* genes (*snR37*, *snR49*, and *snR51*) were significantly down-regulated at 4 h. In the MS300c strain, 1 *snR* gene (*snR76*) was significantly up-regulated at 1 h, and 6 *snR* genes (*snR19*, *snR34*, *snR37*, *snR46*, *snR49*, and *snR190*) were significantly down-regulated at 4 h.

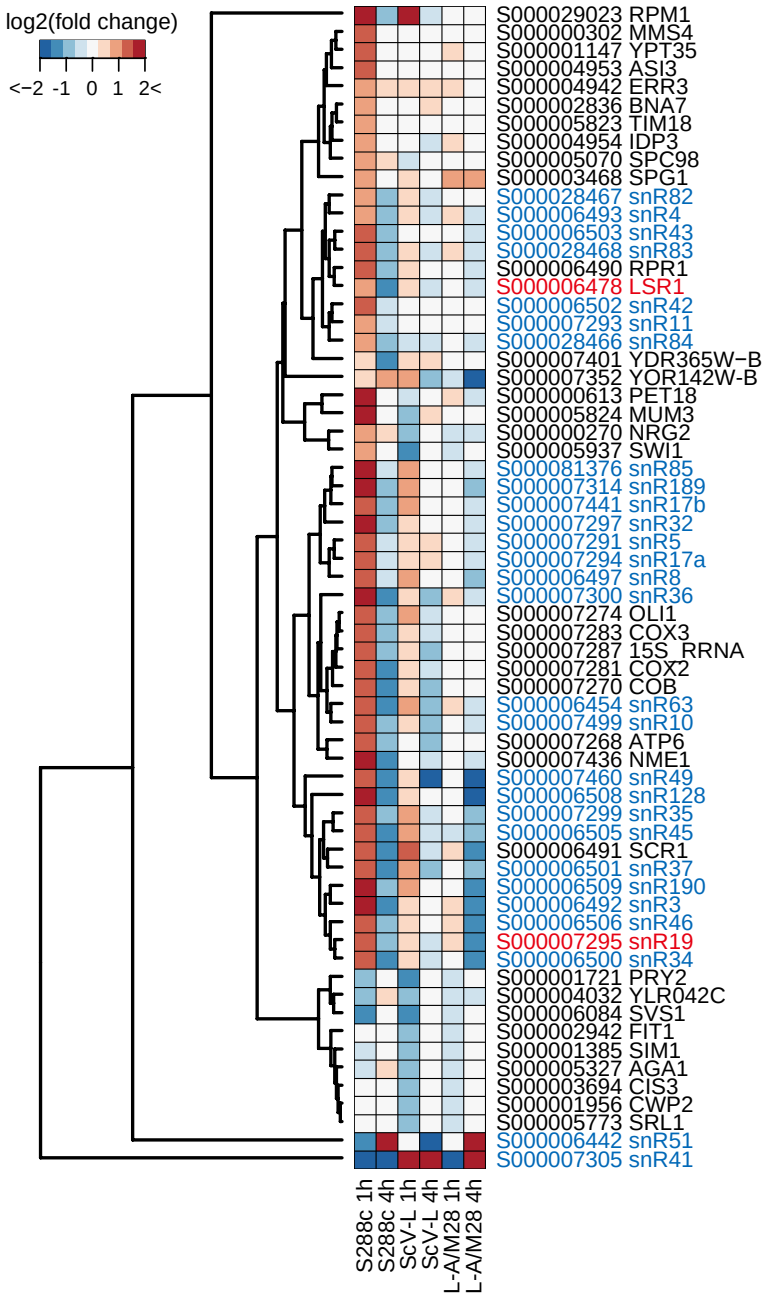


Figure 3-3. Heat map displaying fold changes of transcript levels of the selected DE genes. The genes found in the significantly over-represented full GO terms with more than 3 DE genes detected are shown. The Euclidean distances are shown based on log-transformed fold change values.

Genes in red indicate those encoding small nuclear (sn)RNAs, while genes in blue indicate those encoding small nucleolar (sno)RNAs.

Discussion

A large number of *snR* genes were affected by ribavirin (Figure 3-3). Their transcripts are small nuclear (sn)RNAs or small nucleolar (sno)RNAs, which are non-coding (nc)RNAs localizing to the cell nucleus or nucleolar, respectively. A total of 82 *snR* genes, including 76 and 6 genes encoding snoRNAs and snRNAs, respectively, are known for *S. cerevisiae* (Ashburner et. al., 2000, Gene Ontology, 2015), from which 29 snoRNAs and 2 snRNAs were differentially detected from the samples exposed to ribavirin. Both the box H/ACA and box C/D snoRNAs were differentially detected and significantly enriched into the GO terms such as box H/ACA snoRNP complex (GO: 0031429) and box C/D snoRNP complex (GO: 0031428) in the S288C strain (Tables S3 and S4), while only the box H/ACA snoRNAs were significantly enriched in the S7 and MS300c strains (Tables 3-S5, 3-S8, and 3-S11). Most of the snoRNAs differentially detected are dispersed and transcribed as independent singlets, with the exceptions of polycistronically-encoded clusters of *snR128* and *snR190*, and of *snR41* and *snR51* (Lowe and Eddy, 1999).

The snRNAs and snoRNAs detected in this study are thought to be polyadenylated since RNAs were enriched by an oligo(dT)-based method (see the method section), and a similar purification method has been used to study polyadenylated human mitochondrial RNAs (Szczesny et. al. , 2010). Polyadenylation is known as a way to tag defective ncRNAs, including

snRNAs and snoRNAs, destined for degradation (Reinisch and Wolin, 2007), for which the TRAMP complex interacts with the nuclear exosome of eukaryotic organisms (Egecioglu et. al. , 2006, LaCava et. al. , 2005). However, non-polyadenylated RNAs might be remained in our samples since a large number of mitochondrial (mt)RNAs were differentially detected, which include transcripts of *ATP6*, *RPM1*, *OLI1*, *COX3*, *15S rRNA*, *COX2*, and *COB* (Figure 3 and Table S2), for which polyadenylation has been undiscovered in yeast (Dziembowski et. al. , 2003, Levy and Schuster, 2016). Regardless, however, of the polyadenylation status, the differential detections of snRNAs, snoRNAs, and mtRNAs were systematic based on the term enrichment analysis and therefore indicative of effects of ribavirin on such cellular RNAs.

The majority of the *snR* transcripts increased at 1 h, but decreased at 4 h to the sub-basal levels, and the tendency was reproducible across the three tested strains (Figure 3-3). The tendency was also reproducible based on the results by the term enrichment analysis, with RNA modification guide activity, rRNA binding, nucleolus, RNA modification, and rRNA processing as the five most significant slimmed GO terms for the gene sets up-regulated at 1 h and down-regulated at 4 h in the S288C and S7 strains, and for the gene set down-regulated at 4 h in the MS300c strain (Figure 3-2). Our result suggests that snRNAs and snoRNAs were polyadenylated for the first 1 h and degraded to the sub-basal transcript levels by 4 h of ribavirin exposure. The time scale seems reasonable as literature reported polyadenylated RNA was degraded for a duration of 50 min by the archaeal exosome (Hartung et. al. , 2010). Despite the similar time-course pattern observed across the three

strains, the numbers of the significant *snR* genes were strain-dependent (Table 3-S2). The largest number was observed in the S288C strain, with 29 significant *snR* genes observed at 1 h and/or 4 h. The numbers were smaller in the S7 and MS300c strains, with 5 and 7 significant *snR* genes, respectively.

Ribavirin is a base analogue that is thought to be incorporated into viral RNA by viral RNA-dependent RNA polymerases (Crotty et. al. , 2001). Incorporation of ribavirin molecules into viral RNA is thought to result in chain termination and/or point mutation that leads to inefficient translation of viral transcripts (Bull et. al., 2005, Crotty et. al., 2002, Dietz et. al., 2013, Ortega-Prieto et. al., 2013). Similarly, ribavirin might be incorporated into cellular snRNAs and snoRNAs by the DNA-dependent RNA polymerase II that also involves syntheses of cellular mRNAs. Unlike snRNAs and snoRNAs, however, matured cellular mRNAs are polyadenylated on which effects of ribavirin are invisible based on polyadenylation status by mRNA-Seq. Our result suggests a possibility of incorporation of ribavirin into cellular RNAs by DNA-dependent RNA polymerases.

Meanwhile, no difference was observed in the numbers of variant callings in the *snR* transcripts between the samples exposed to ribavirin and the respective negative controls (Table 3-S12), suggesting point mutation was not a mechanism responsible for affecting snRNAs and snoRNAs in yeast exposed to ribavirin. At present, we do not know the mechanisms. One possibility is that ribavirin molecules might be incorporated into snRNAs and snoRNAs, but they were not detected as base substitutions if they were correctly reverse-transcribed into cDNAs for the analyses by mRNA-Seq.

The ribavirin-containing snRNAs and snoRNAs might be structurally aberrated and therefore preferentially polyadenylated since the TRAMP complex can discriminate misfolded forms of ncRNAs (Vanacova et. al. , 2005). Alternatively, the aberrated snRNAs and snoRNAs might be preferentially degraded because they were not sequestered and protected from the nucleus exosome by specific RNA-biding proteins of small nuclear ribonucleoproteins (snRNPs) and small nucleolar (snoRNPs) (Reinisch and Wolin, 2007). Each snRNA or snoRNA molecule assembles with protein molecules to form a snRNP or a snoRNP, respectively. The aberrated snRNAs and snoRNAs might be incorrectly assembled into RNPs, and therefore unprotected from a scavenger pathway of the TRAMP complex (Reinisch and Wolin, 2007).

snRNPs have functions in processing pre-mRNA in the nucleoplasm (Matera et. al., 2007), whereby snoRNPs have functions in guiding chemical modifications of other RNAs such as ribosomal RNAs, transfer RNAs, and snRNAs (Kiss, 2001, Tollervey and Kiss, 1997). Our term enrichment analyses confirm such functions were significantly affected by exposure to ribavirin in yeast (Figure 2, Tables S3-S5, S8 and S11). Small RNPs, including snRNPs and snoRNPs, are known to be associated with human diseases such as spinal muscular atrophy, dyskeratosis congenital, and Prader-Willi syndrome (Matera et. al., 2007). Literature reported hematologic, dermatologic, and neuropsychiatric disorders in patients with HCV infection treated with Peg-IFN and ribavirin (Sulkowski et. al., 2011). Our study revealed ribavirin affected snRNPs and snoRNPs in yeast. There may be a need to scrutinize the relationships between such disorders and

small RNPs in patients who are treated with ribavirin. This chapter found antiviral ribavirin affected small non-coding RNAs in yeast, which may be significant when considering side effects in humans who are treated for viral infections by ribavirin.

CHAPTER IV.

Characterization of effects of nitazoxanide on whole transcriptomes of *S. cerevisiae* strains containing dsRNAvirus-like particles and cured strains by RNA-Seq.

Introduction

Nitazoxanide (NTZ), 2-acetyloxy-*N*-(5-nitro-2-thiazolyl) benzamide , is a broad-spectrum anti-infective drug that markedly modulates the survival, growth, and proliferation of a range of extracellular and intracellular protozoa, helminths, anaerobic bacteria (Fox and Saravolatz, 2005). Recently, it has been studied as a broad-spectrum antiviral agent due to its ability to inhibit the replication of several RNA and DNA viruses, such as influenza virus, rotavirus and norovirus (La Frazia et. al., 2013, Rossignol, 2014). It is in Phase II/III clinical trials for the treatment of influenza and is also being researched as a potential treatment for chronic hepatitis B, chronic hepatitis C, rotavirus and norovirus gastroenteritis (Rossignol, 2014). However, its antiviral mechanisms have not been fully understood. Several potential antiviral mechanisms have been reported such as activation of innate immune response, downregulation of viral receptors or interfere with maturation of the viral hemagglutinin glycoprotein at the post-translational stage probably due to ATP-sensitive intracellular Ca^{2+} depletion resulting in mild endoplasmic reticulum (ER) stress (Ashiru et. al. , 2014, Elazar et. al. , 2009, Gekonge et. al. , 2015, La Frazia et. al., 2013, Rossignol, 2009, Trabattoni et. al. , 2016). No major side effects of nitazoxanide have been reported until now. Therefore, from the drug safety and mechanisms side, effects of nitazoxanide need to be further studied at cellular and whole genome levels.

As nitazoxanide is a potential broad-spectrum antiviral drug being utilized in the future, it is necessary to know its effects before it reaching to the

antiviral markets. There is so far no next-generation sequencing (NGS) based transcriptomic analysis for effects of nitazoxanide on eukaryotic organisms especially at their whole genome levels, this study aimed to characterize the effects of nitazoxanide on whole transcriptomes of *S. cerevisiae* strains containing dsRNA virus-like particles by RNA-Seq. *S. cerevisiae* was used as a model system in this study due to the fact that it is frequently used as an excellent model system for identifying and studying new drugs targets before applying to human (Bolotin-Fukuhara et. al. , 2010). *S. cerevisiae* strains have been employed for the production of human medicines such as insulin, human serum albumin, hirudin and vaccines employed in the hepatitis B and cancer prevention (Ardiani et. al. , 2010, Nielsen, 2013, Hou et. al. , 2012).

Materials and Methods

Preparation of the tested strains

Four *S. cerevisiae* strains (Table 2-2) of ATCC 44828 (S7) (MATα *DET1-1* [L-A-HN L-(BC)]) (Oliver et. al., 1977, Wickner, 1983), ATCC 201204 (MS300c) (MATa *leu2 ura3-52 ski2-2* [L-A L-BC (L-28) M-28]) (Schmitt et. al., 1996), ATCC 204508 (S288C) (MATα *SUC2 mal mel gal2 CUP1 flo1 flo8-1 hap1*) (Sherman, 2002) and ATCC 201204 (-) (MS300c-) (cured strain originated from killer strain MS300c) were tested.

Nitazoxanide exposures

Each strain was cultured on a yeast peptone dextrose (YPD) (Becton, Dickinson and Company, Sparks, MD, USA) agar plate at 30°C for 48 h, and a single colony of each strain was picked and suspended in 10 ml saline

(0.85%) with Tween 20 (1%). The concentrations of yeast in the suspensions were determined by OD method. The suspensions were inoculated in 4.5 ml of YPD broth with the initial concentration adjusted at 2.5×10^5 CFU ml^{-1}. The inocula were incubated at 30°C by gently shaking using an orbital shaker (SLRM-3, Seoul in Bioscience, Seoul, Korea) for 16 h.

After 16-h incubation, 0.5 ml solution of 100 μg ml^{-1} nitazoxanide (CAS 55981-09-4; Sigma-Aldrich, St. Louis, MO, USA) in 1% DMSO (Sigma-Aldrich) was added to each of the 4.5 ml cultured suspensions, which resulted in final concentrations of 10 μg ml^{-1} of nitazoxanide and 0.1% of DMSO. 10 μg ml^{-1} of nitazoxanide concentration was selected based on a previous finding of 10 μg ml^{-1} as a peak concentration of its hydrolyzed metabolite in human plasma after receiving a single 500-mg oral dose (Broekhuysen et. al., 2000). Only 0.5 ml solution of 1% DMSO was added to negative controls. The samples were incubated at 30°C with agitation for 1 or 4 h after the addition of nitazoxanide in 1% DMSO or 1% DMSO only. The samples were harvested by centrifugation at 10,000 g for 10 min, weighed, and snap-frozen in liquid nitrogen for RNA extraction. Biological triplicates were taken on three different days for each strain.

RNA extraction and sequencing

RNA extraction and sequencing were performed as described (Xu and Yamamoto, 2017). Briefly, total RNA was extracted from 50–100 mg (wet weight) of each sample. About 1 μg of total RNA from each sample was used to purify poly(A)-containing RNA by the TruSeq mRNA Sample Prep

kit v2 (Illumina, Inc., San Diego, CA, USA). The purified and fragmented poly(A)-containing RNA was primed with random hexamers to synthesize first strand cDNA. Double-stranded cDNA was synthesized and purified by the Agencourt AMPure XP kit (Beckman Coulter, Inc., Pasadena, CA, USA). Index adapters were attached to the cDNA, enriched, and quantitated by qPCR and the LabChip GX HT DNA High Sensitivity Kit (PerkinElmer, Waltham, MA, USA). Indexed libraries were treated with the HiSeq PE (Paired-End) Cluster Kit v3 cBot and the TruSeq SBS v3-HS kit (Illumina). Paired-end (2 × 100 bp) sequencing was performed by Illumina HiSeq 2000. Raw sequences were uploaded to the BioProject database of the NCBI under accession number SRP158949.

Sequence data processing and analyses

Both forward and reverse reads after removing the adapter and low quality sequences were mapped against the reference genome of *S. cerevisiae* S288C (GCF_000146045.2) by using the Tophat version 2 with default parameters (Trapnell et. al., 2009).The fragments per kilobase of exon per million reads mapped (FPKM) values were calculated, and differentially expressed (DE) genes were determined by the pooled modeof the Cuffdiff in Cufflinks package version 2.1.1 (Trapnell et. al., 2010). DE genes were based on biological triplicates of each nitazoxanide exposed sample relative to biological triplicates of respective negative controls exposed to 0.1% DMSO only. The DE genes were defined when uncorrected *p*-value was greater than the FDR adjusted *p*-value (*q*-value) after Benjamin-Hochberg correction for multiple-testing. The full and slimmed gene ontology (GO)

terms were determined for the DE gene sets for each sample by the Cytoscape (Shannon et. al., 2003) plugin the BiNGO version 3.0.3 (Maere et. al., 2005) against the GO annotation file for *S. cerevisiae* S288C genome, i.e., gene_association.sgd, submitted on March 1, 2018 to the Gene Ontology Consortium (Gene Ontology, 2015, Ashburner et. al., 2000). The up- and down-regulated genes were analyzed separately (Hong et. al., 2014). The hypergeometric test was used. Enrichment of differentially regulated genes in KEGG (Kyoto Encyclopedia of Genes and Genomes) pathways was determined using DAVID Bioinformatics Resources 6.8 (Huang da et. al. , 2009b, Huang da et. al. , 2009a).

Quantitative real-time RT-PCR

Quantitative real-time RT-PCR was performed to confirm the expression of mRNAs by RNA-Seq analysis. There is an argument about if qPCR is necessary for RNA-Seq validation. Opinions are diverse. However, it is always necessary to validate functionally the selected potential genes obtained from RNA-Seq for the given trait. Since this study narrowed down the analysis for some exact candidate genes (human disease related), the qPCR validation step was conducted here. Reverse transcription of the RNA samples was performed as previously described (Teste et. al. , 2009). Briefly, total RNA from each sample that shared the same treatment with RNA-Seq experiment were reverse transcribed into cDNA in a 20 μL reaction mixture using the iScript cDNA synthesis kit (Bio-Rad). Primers for 7 genes were designed and synthesized (Table 4-1). The PCR efficiency of each primer pair was calculated based on the slope of the standard curve by the dilution

series method using a mix of sample cDNAs as the template. The expression level of gene UBC6 were stable among samples of RNA-Seq and were therefore chosen as the internal reference for the normalization of gene expression (Vandesompele et. al. , 2002). Then, qPCR was performed using QuantStudio 6 Flex Real-Time PCR System (Applied Biosystems). The 20 μL PCR reactions included 10 μl Fast SYBR Green Master Mix (2×) (Applied Biosystems), forward and reverse primer with 200nM final concentration and cDNA template. The reactions were follow the condition as 95 ℃ for 15 min of initial denaturation and 45 cycles of 95 ℃ for 15 s of dissociation and 60 ℃ for 1 min of annealing and extension. All reactions were run in triplicate. After reaction, the expression levels of the genes were measured in terms of threshold cycle value (CT), and then normalized to UBC6 using –[delta][delta] CT (Livak and Schmittgen, 2001).

Table 4-1. List of reference gene and genes of interest.

Gene short name	Molecular Function (SGD curated)	Primer sequences	Eff
UBC6	Ubiquitin-protein transferase activity	F:GATACTTGGAATCCTGGCTGGTCTGTCTC R:AAAGGGTCTTCTGTTTCATCACCTGTATTTGC	87
UTP4	Unknown	F: ACAGAATGGGATTTAGCAACAG R: TCAGAACAACCACCAATCAC	81
UTP6	snoRNA binding	F: CCCTGATGTGCCTAAGCTATG R: TACGCTGATGTCTGCCTCTG	90
UTP14	Unknown	F: CGAGGAAGAGACGAATGGAG R: CCACAATTATTGCGCCTTCT	87
UTP21	Unknown	F: AGCAATTACGAGAGGGCTCA R: TCACCGTGTGCCTTAAACAG	81
NOP4	RNA binding/mRNA binding	F: GATGGGCTTAAGGTGGTTGA R: GGATTCTCCGACATCTCCAG	71
IMP3	snoRNA binding	F: GAATGGAAGCAGGACCAAG R: ACGAAATGGATCAGTGGGAG	83

F: forward primer; R: reverse primer. Eff: PCR application efficiency

Results

Sequencing statistics and summary

For each library, 9,552,706 to 15,968,332 sequences were mapped to the reference genome of *S. cerevisiae* S288C, representing 77- to 129-fold coverages of redundancy according to the equation given by Lander and Waterman (1988) (Table 4-1). A total of 5,940 transcribed genes were detected, representing 94% of the 6,350 known genes of the *S. cerevisiae* S288C strain.

The mean FPKM values of the biological triplicates of each transcribed gene for each sample are shown in Figure 4-1. A total of 2378 DE genes were detected (Table 4-A1 to 4-A4), with the number ranging from 22 to 626 for the up-regulated genes and from 3 to 526 for the down-regulated genes for samples exposed to ribavirin relative to basal transcript levels in the respective negative controls exposed to 0.1% DMSO only (Figure 4-2). There are more DE genes (both up and down-regulated) at 4 h than at 1 h for strains S7, MS300c and MS300c-. While for strain S288C, there are considerable DE genes at 1 h, though relatively less than DE genes at 4 h.

Table 4-2. Number and coverage of cDNA sequences in the three *S. cerevisiae* strains.

Strain	Type	Time (h)	Replicate	Total reads [a]	Mapped reads [b]	Fraction of mapped reads (%)	Coverage [c]
ATCC 204508	Control	1	1	13704575	12863686	93.7	104.9
(S288C)			2	15865960	14918943	93.9	121.6
			3	14548138	13522715	92.7	109.9
		4	1	12963352	12195506	93.9	99.4
			2	15795789	14920435	94.3	121.7
			3	14936927	13904661	92.9	113.0
	Exposed	1	1	13595656	12830733	94.2	104.6
			2	13527247	12638256	93.2	103.2
			3	15739532	14635914	92.7	119.1
		4	1	13172961	12443800	94.3	101.5
			2	15047082	14136541	93.7	115.3
			3	13820363	12894734	93.1	104.8
ATCC 44828	Control	1	1	11401152	10569941	92.1	86.1
(S7)			2	15043187	13856298	91.9	112.9
			3	14591670	13327924	91.0	108.2
		4	1	12399830	11250266	90.5	91.7
			2	14109327	12732683	90.0	103.8
			3	15158945	13561356	89.3	110.2
	Exposed	1	1	15991466	14919983	93.0	121.6
			2	16085197	14913592	92.4	121.6
			3	14356492	13071984	90.7	106.0
		4	1	15319844	13924762	90.7	113.5

			2	14003567	12799260	91.2	104.3
			3	14028368	12643283	89.9	102.7
ATCC 201204 (MS300c)	Control	1	1	16442321	14335062	87.0	116.9
			2	13374297	10493697	78.3	85.3
			3	14783245	11559996	78.0	93.9
		4	1	13523465	10244957	75.6	83.6
			2	15999567	10603369	66.2	86.1
			3	15089487	10004417	66.1	81.3
	Exposed	1	1	11108051	9552706	85.8	77.9
			2	13665170	10920824	79.7	88.7
			3	18824211	14429830	76.5	117.3
		4	1	13108182	10034858	76.4	81.8
			2	16459004	12497543	75.8	101.6
			3	13694402	10691362	77.9	86.9
ATCC 201204(-) (MS300c-)	Control	1	1	11593811	10876323	93.6	88.6
			2	15852376	14782525	93.0	120.0
			3	13994399	12969624	92.5	105.4
		4	1	16808545	15766892	93.5	128.6
			2	15428197	14325867	92.6	116.4
			3	14771838	13742912	92.7	111.7
	Exposed	1	1	13378530	12603757	94.0	102.7
			2	15506219	14521296	93.4	118.0
			3	13901117	12876259	92.4	104.5
		4	1	14696835	13855696	94.0	113.0
			2	14862689	13801777	92.6	112.1

	3	17125616	15968332	92.9	129.7

[a] The number of the pairs of forward and reverse sequence reads after quality trimming.

[b] The number of the pairs of forward and reverse sequence reads mapped to the reference genome of S288C by the Tophat2.

[c] The coverages were estimated by the equation given by Lander and Waterman (1988) and derived by dividing the number of total read bases by the average haploid genome size of *S. cerevisiae* S288C (24.991364 Mb).

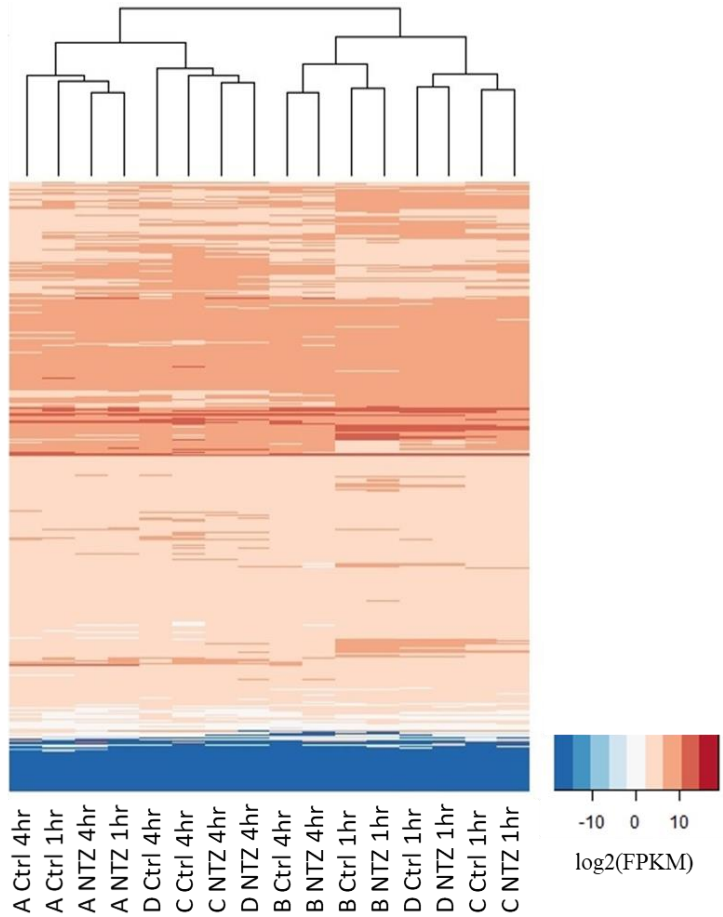


Figure 4-1. Global transcriptomes of the S288C, S7, MS300c and MS300c-*S. cerevisiae* strains. A: S288C strain; B: S7 strain; C: MS300c strain; D: MS300c- strain. The Euclidean distances are shown based on log-transformed FPKM values of all 5,940 transcribed genes.

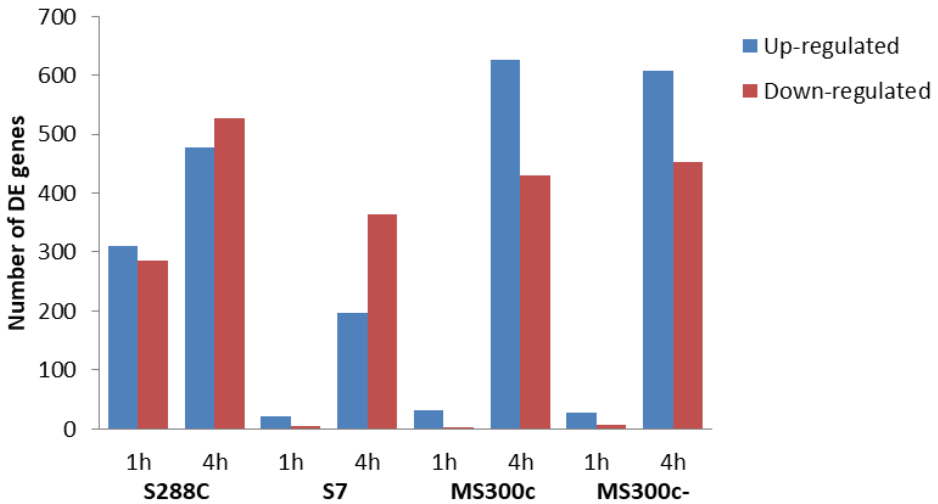
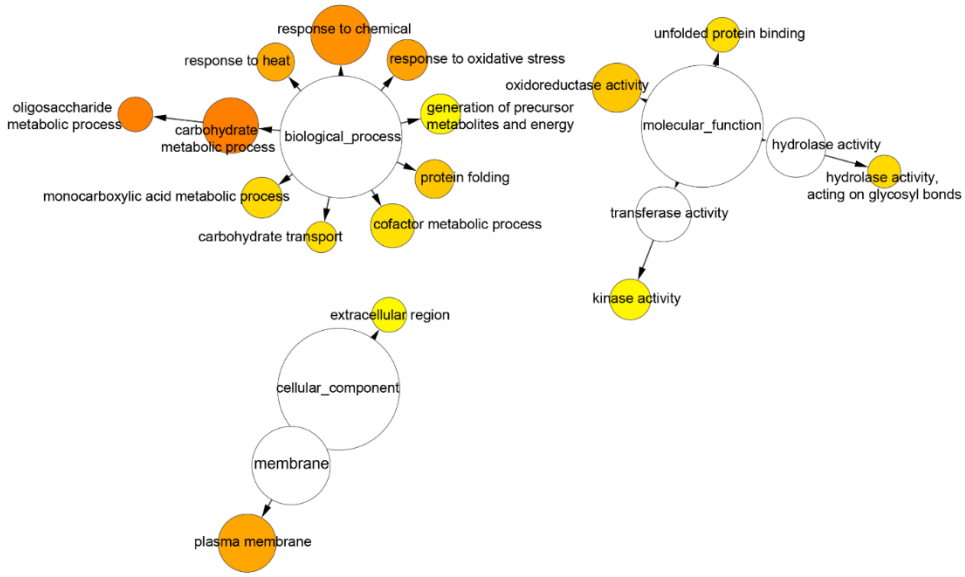


Figure 4-2. Number of DE genes relative to the respective controls exposed to 0.1% DMSO only.

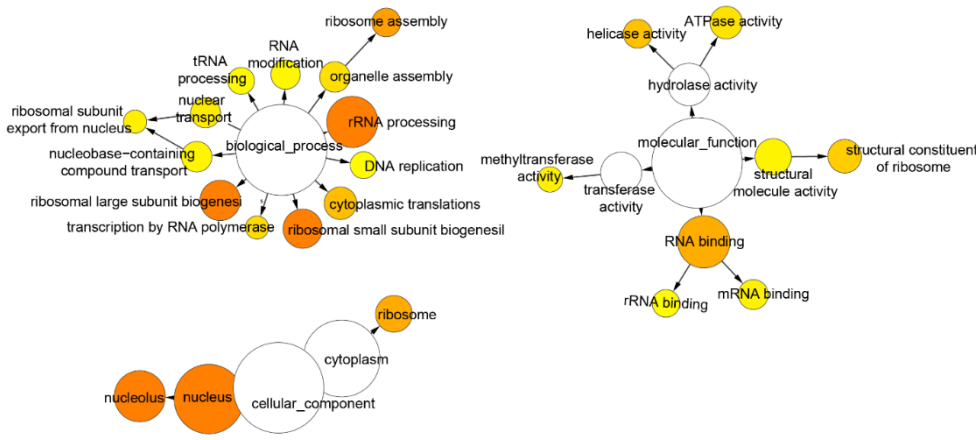
GO terms and KEGG pathways

To understand the functions of DE genes and the biological pathways involved in nitazoxanide exposure, the significantly over-represented GO terms and KEGG (Kyoto Encyclopedia of Genes and Genomes) pathways were determined based on the up-regulated and down-regulated gene sets for each strain at each time point. The slimmed GO terms are shown in Figure 4-3. No slimmed GO term was found for the gene sets at 1 h in the S7 and MS300c strains and down-regulated at 1 h in MS300c- strain. The six significantly commonly presented slimmed GO terms among four strains were ribosome assembly (GO: 0042255), ribosomal small subunit biogenesis (GO: 0042274), ribosomal large subunit biogenesis (GO: 0042273), rRNA processing (GO: 0006364), nucleolus (GO: 0005730) and plasma membrane (GO: 0005886) (Figure 4-3). There are 6 out of 20, and 9

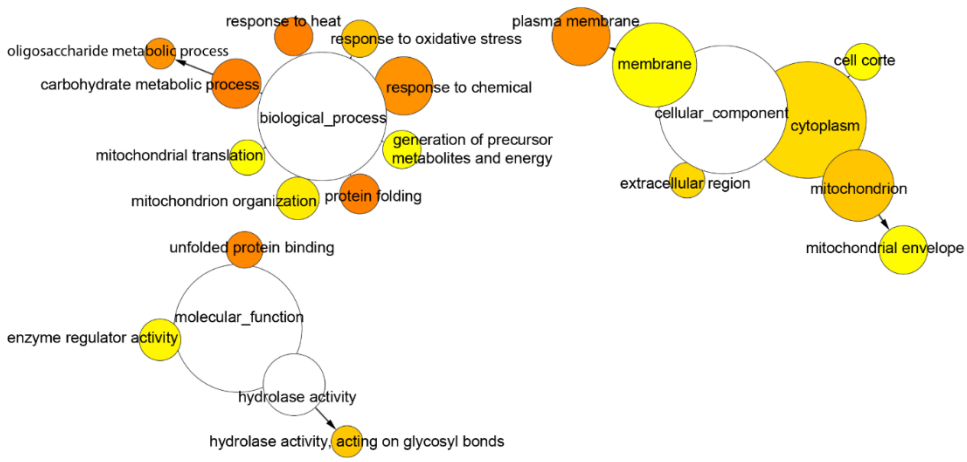
out of 21 GO terms based on gene set up-regulated at 4 h in the strain S288C and strain S7, were found also in the GO terms based on the gene set down-regulated at 4 h in the strain MS300c. The similar tendency was found for the S288C and S7 strain compared to MS300c- strain (Figure 4-3). The full GO terms are listed in Tables 4-A5 to Table 4-A18. KEGG pathways analyses then conducted to assign functional meanings to genes. Enrichment *p*-values, % of pathway coverage, and number of contributing responsive genes are summarized in Table 4-A19 to Table 4-A25. As shown in Figure 4-4, there were totally four main categories: genetic information processing, metabolism, cellular processes and environmental information processing for four different strains. Enrichment for ribosome biogenesis in eukaryotes (03008), biosynthesis of antibiotics (01130), starch and sucrose metabolism (00500), biosynthesis of secondary metabolites (01110), metabolic pathways (01100), biosynthesis of amino acids (01230), pyruvate metabolism (00620) and 2-Oxocarboxylic acid metabolism (01210) was recurring across four different strains. Pathways of ribosome (03010), RNA polymerase (03020), purine metabolism (00230), citrate cycle (TCA cycle) (00020), carbon metabolism (01200), glyoxylate and dicarboxylate metabolism (00630), meiosis-yeast (04113) and cysteine and methionine metabolism (00270) were enriched across three strains of the tested four strain.



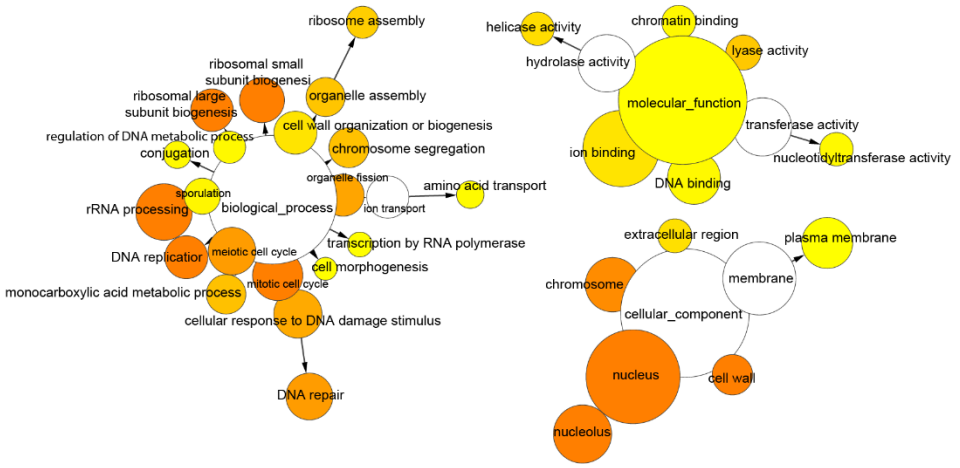
(a) S288C up 1hr



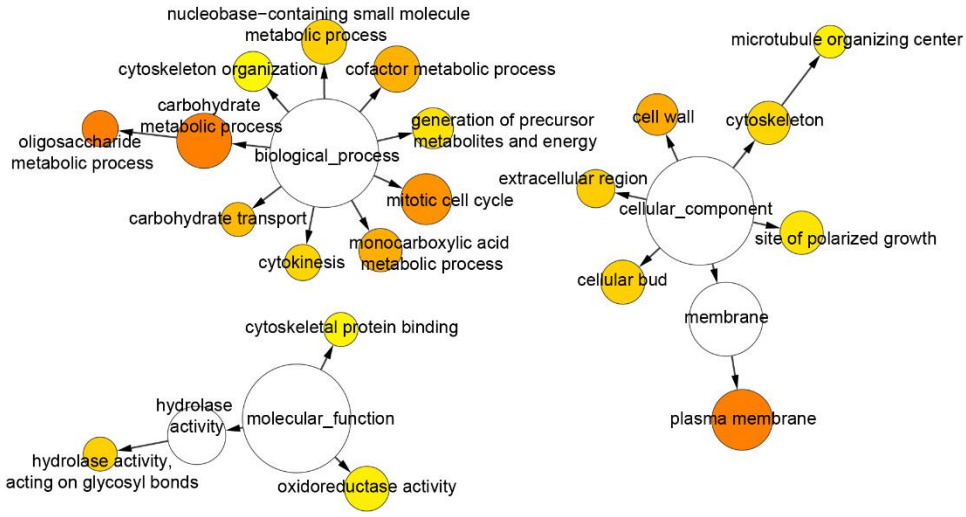
(b) S288C down 1hr



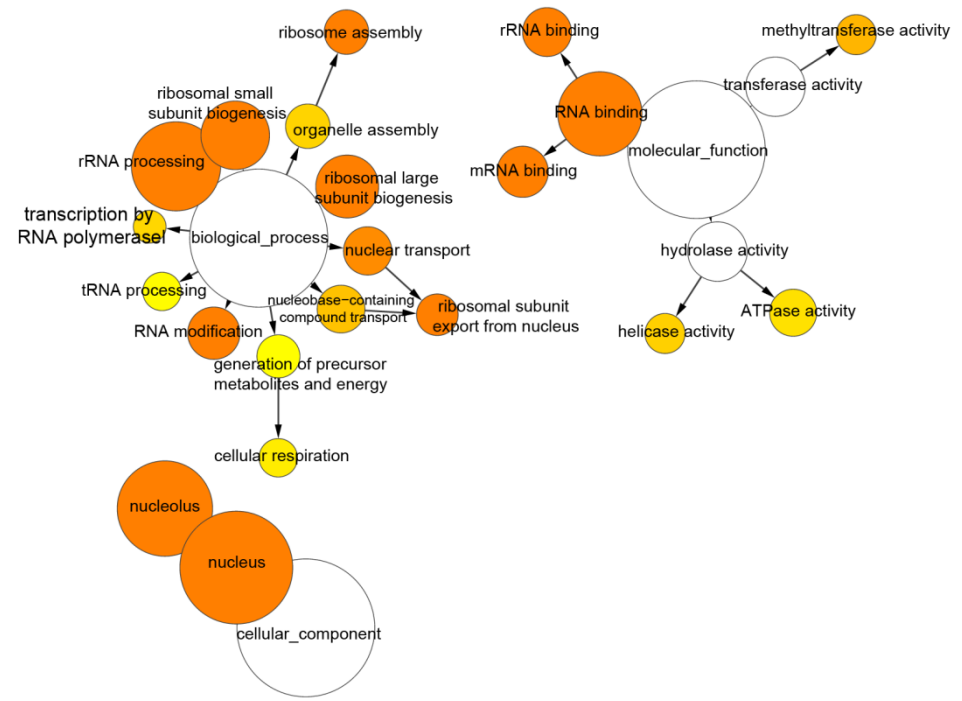
(c) S288C up 4hr



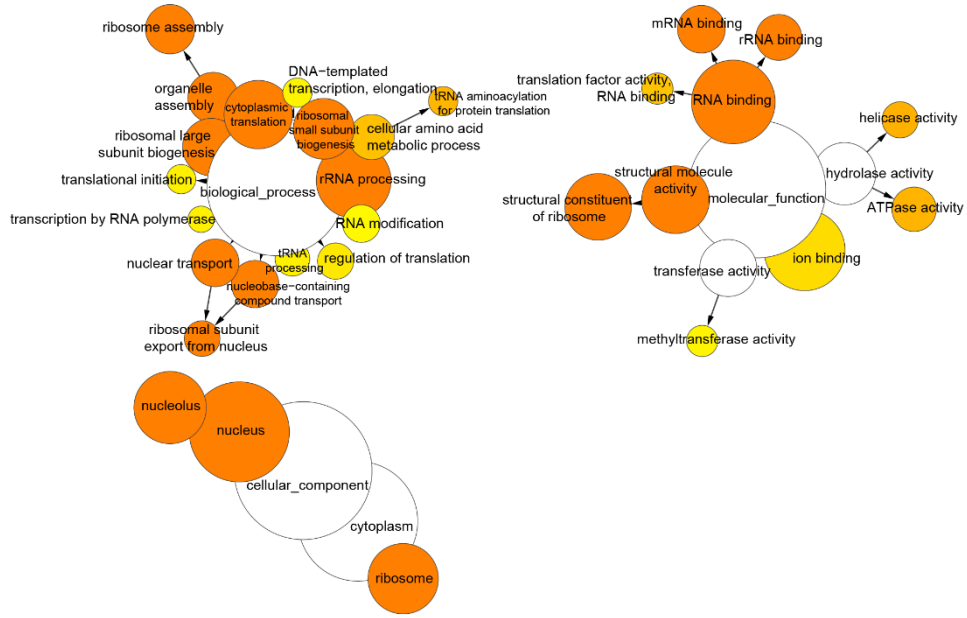
(d) S288C down 4hr



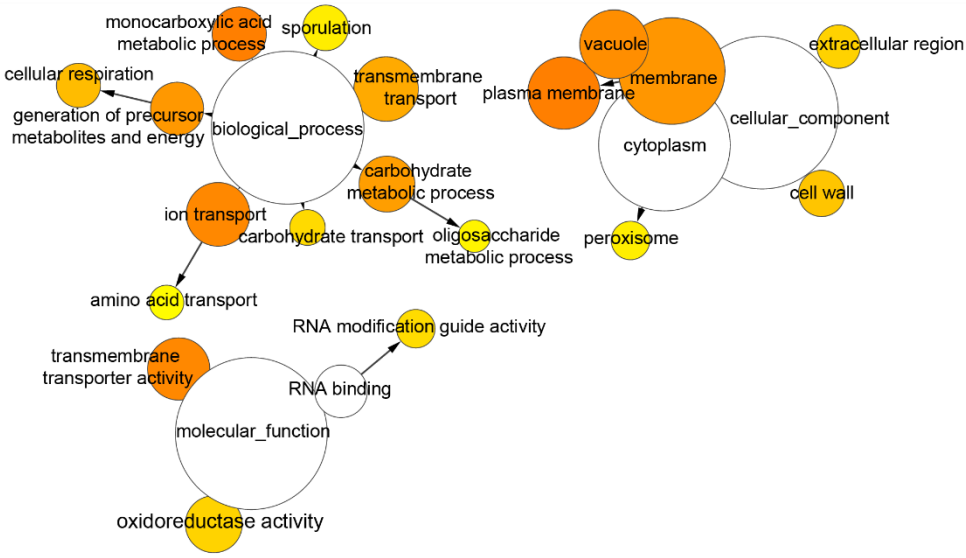
(e) S7 up 4hr



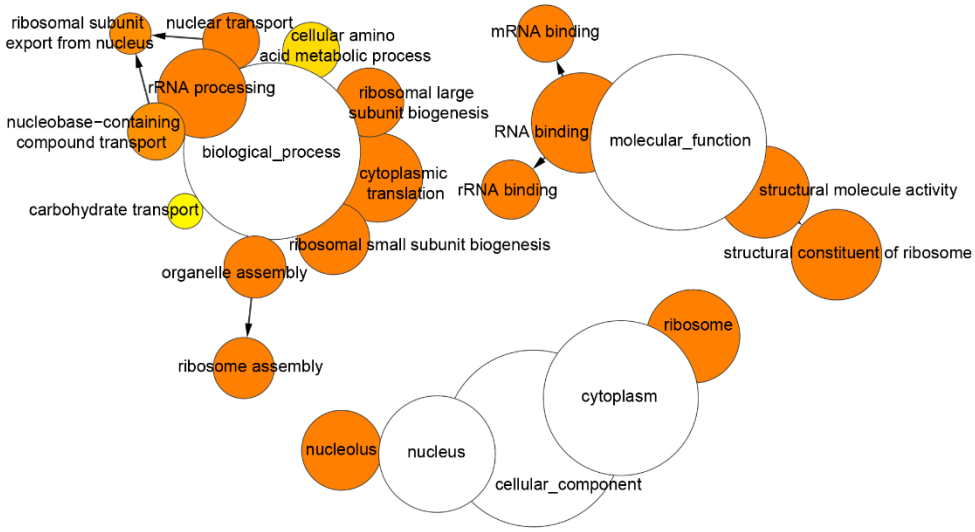
(f) S7 down 4hr



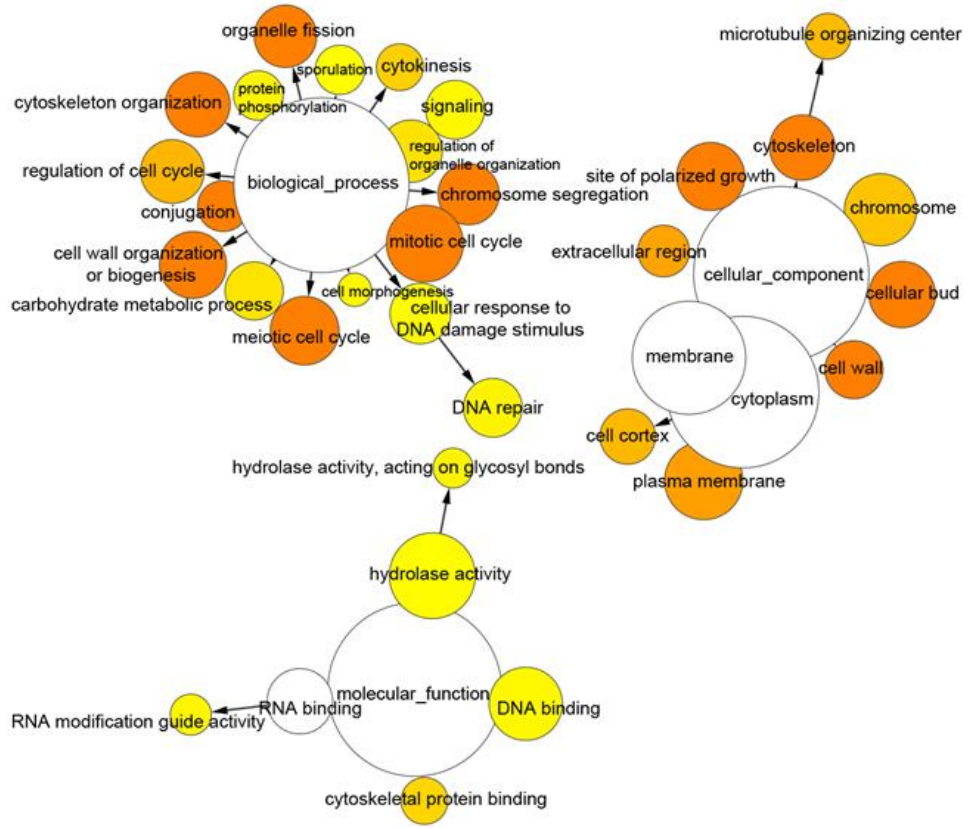
(g) MS300c up 4hr



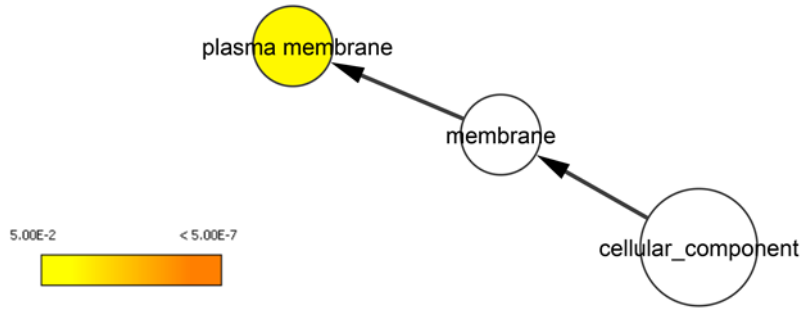
(h) MS300c down 4hr



(i) MS300c- up 4hr

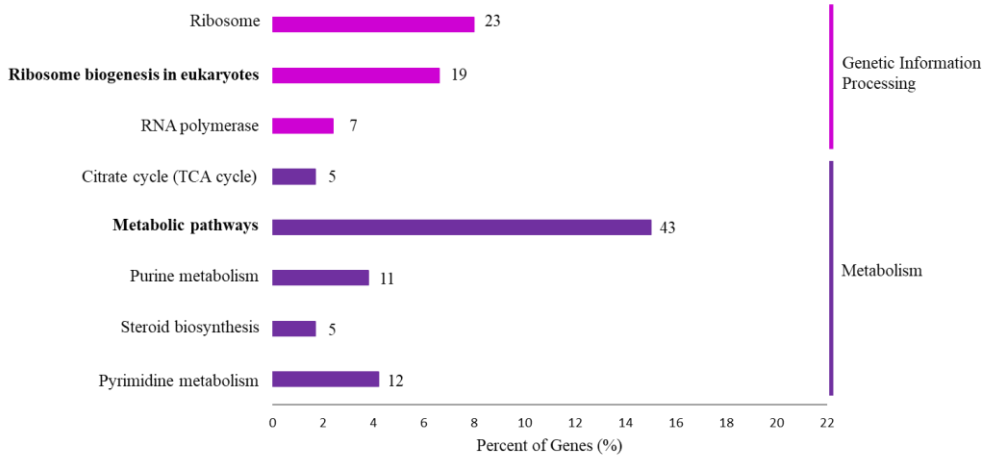


(j) MS300c- down 4hr

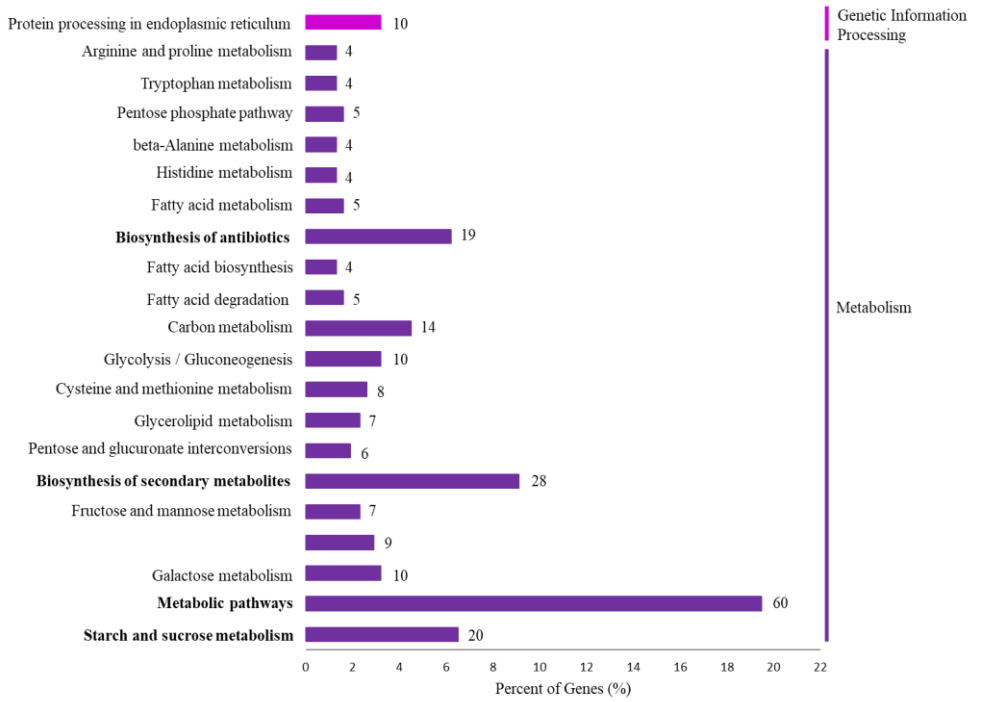


(k) MS300c- up 1hr

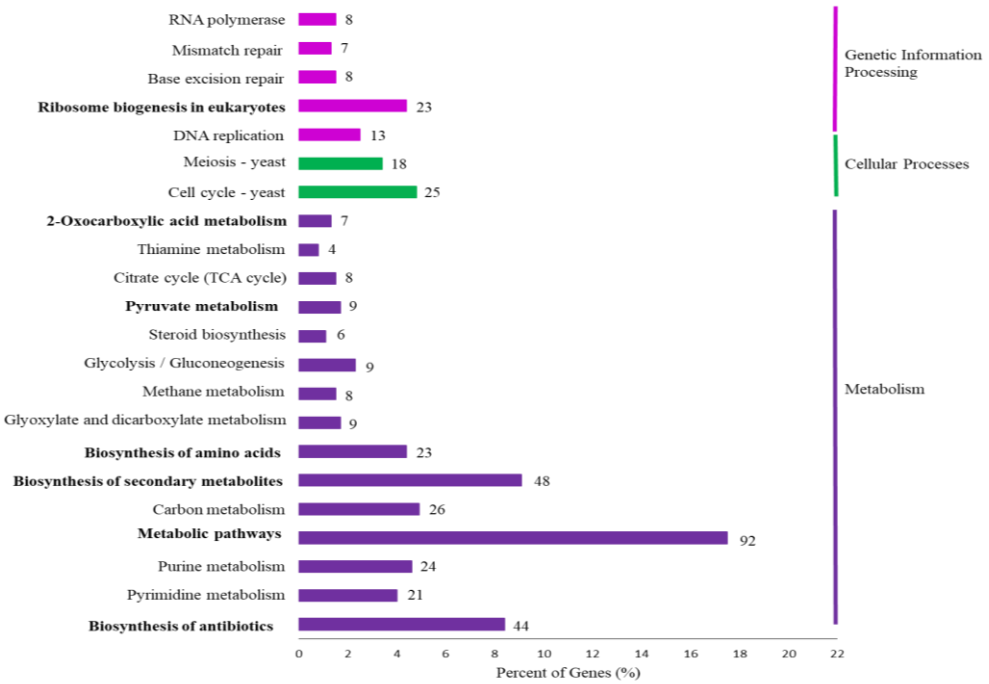
Figure 4-3. Slimmed GO terms based on the DE gene sets (a) up-regulated at 1 h in the S288C strain, (b) down-regulated at 1 h in the S288C strain, (c) up-regulated at 4 h in the S288C strain, (d) down-regulated at 4 h in the S288C strain, (e) up-regulated at 4 h in the S7 strain, (f) down-regulated at 4 h in the S7 strain, (g) up-regulated at 4 h in the MS300c strain, (h) down-regulated at 4 h in the MS300c strain, (i) up-regulated at 1 h in the MS300c- strain, (j) up-regulated at 4 h in the MS300c- strain, (k) down-regulated at 4 h in the MS300c- strain. The size of each node is proportional to the expected number of genes in each GO term. The connection between each node represents hierarchy of GO terms. Yellow to orange colors indicate nodes with statistical significance (*p*-values). Nodes in white are not significantly overrepresented. No slimmed GO term was found for the samples that are not shown in this figure.



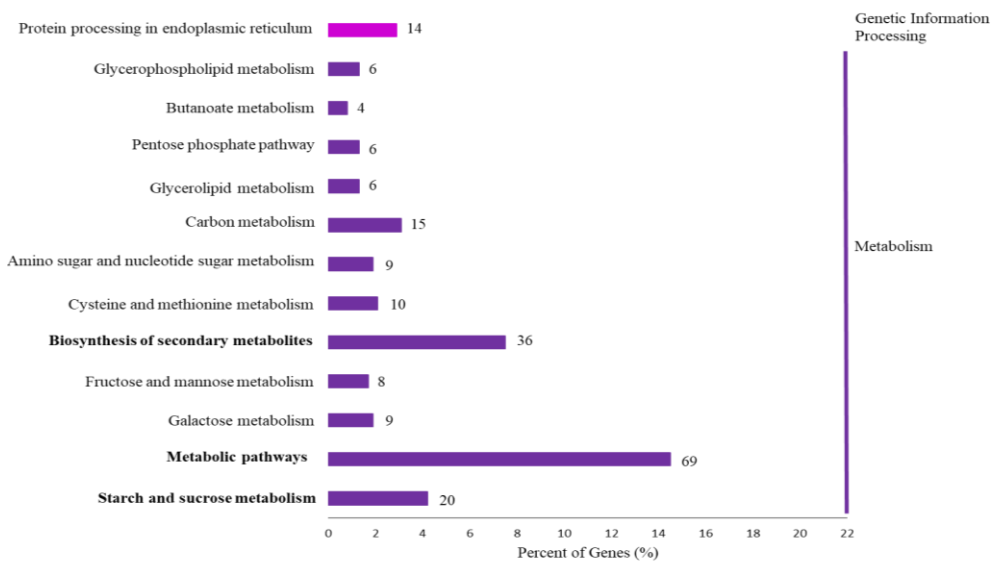
(a) Pathways for genes down-regulated at 1 h in S288C strain



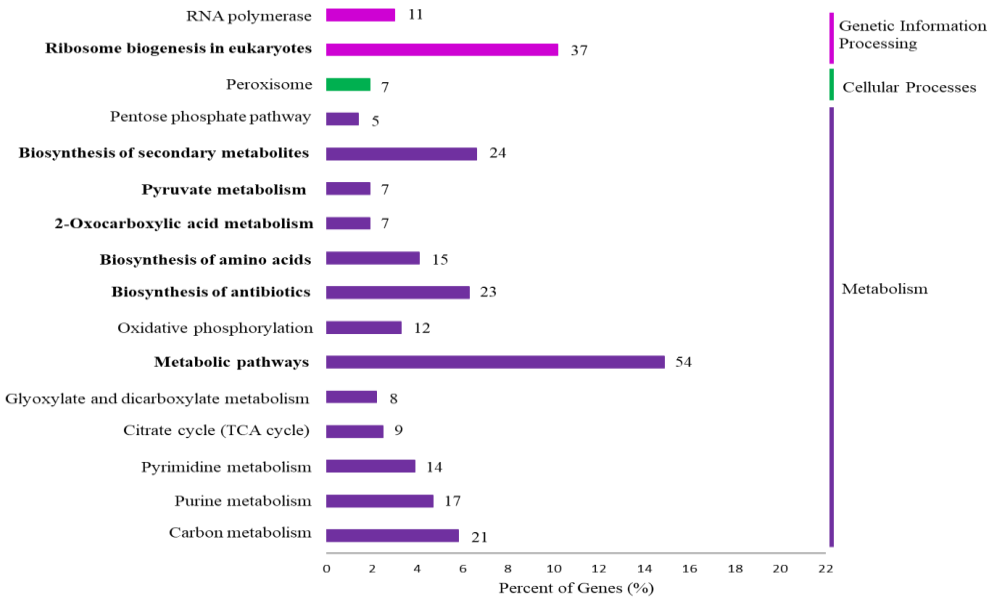
(b) Pathways for genes up-regulated at 1 h in S288C strain



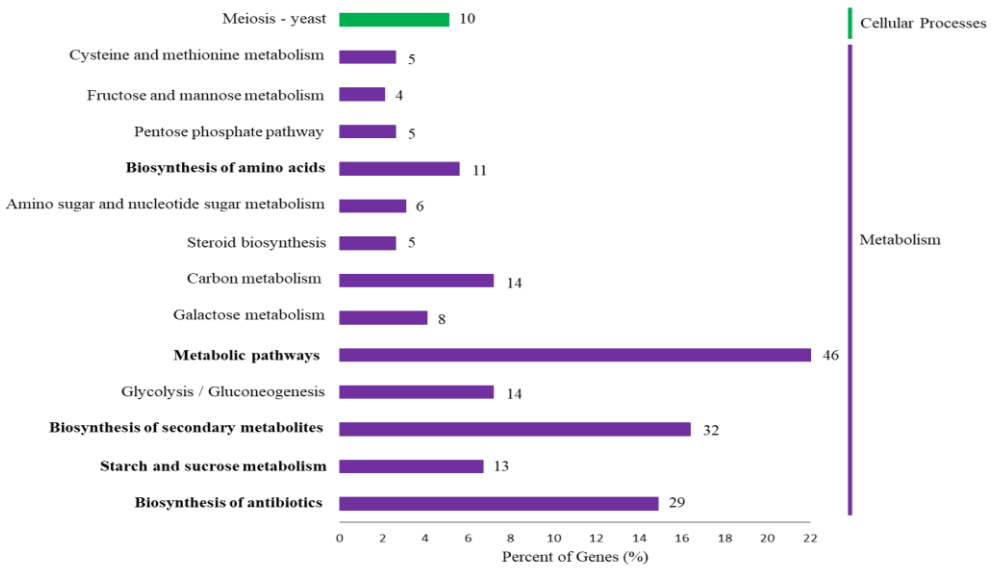
(c) Pathways for genes down-regulated at 4 h in S288C strain



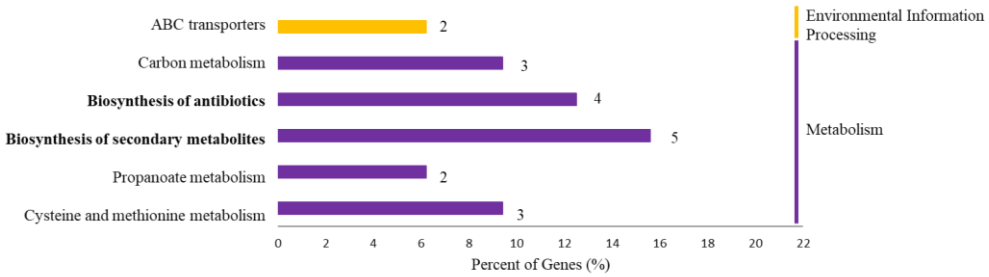
(d) Pathways for genes up-regulated at 4 h in S288C strain



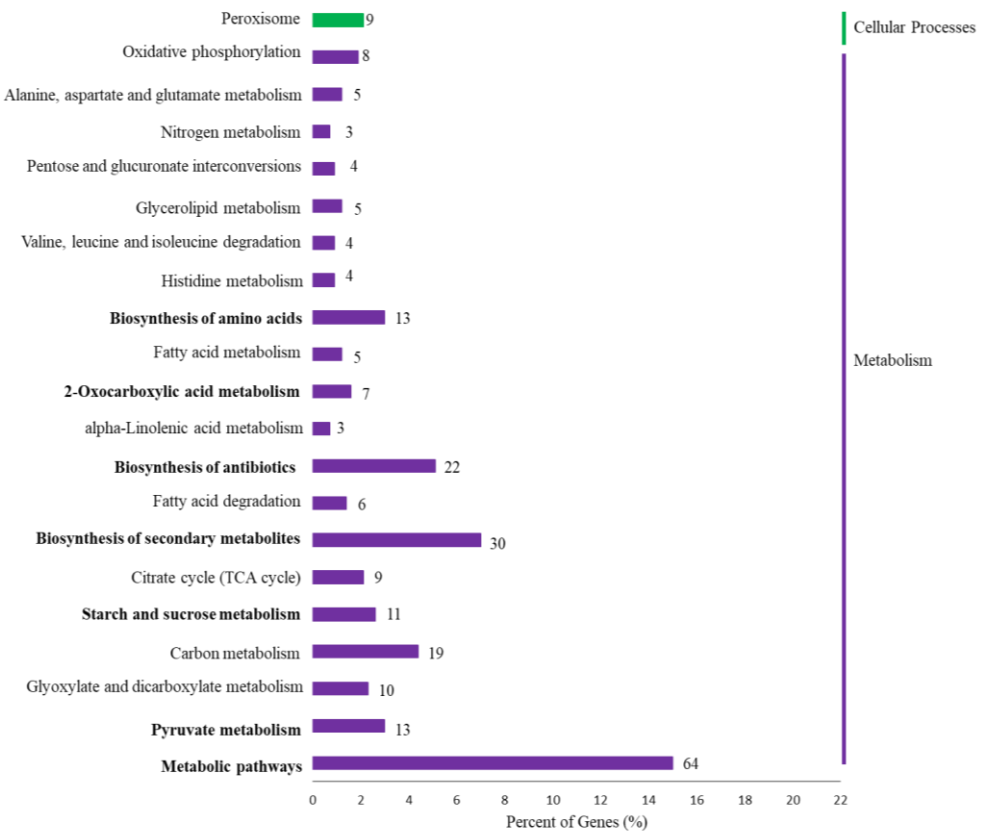
(e) Pathways for genes down-regulated at 4 h in S7 strain



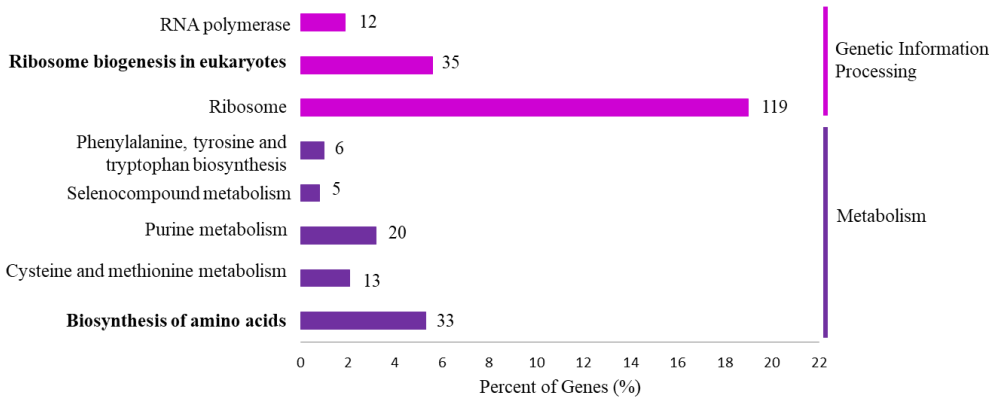
(f) Pathways for genes up-regulated at 4 h in S7 strain



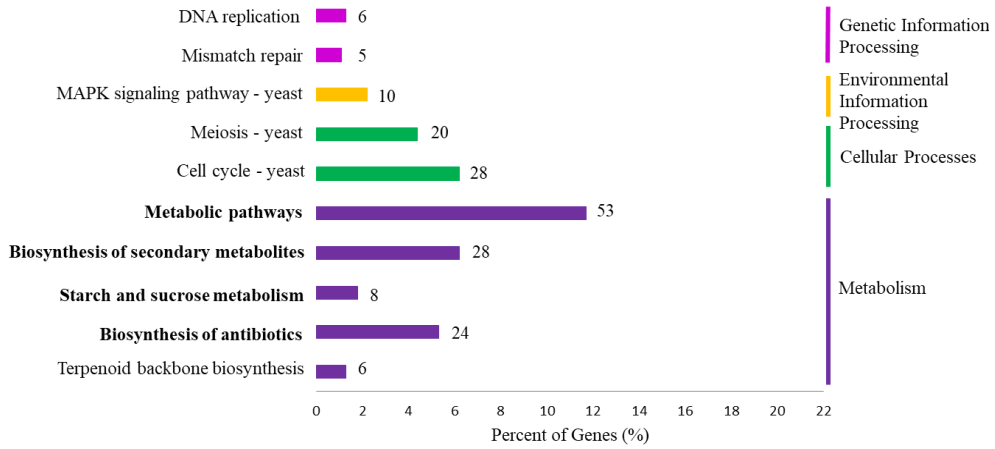
(g) Pathways for genes up-regulated at 1 h in MS300c strain



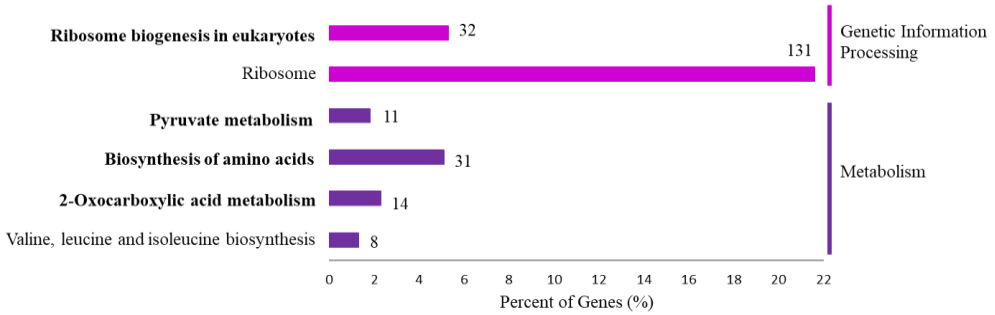
(h) Pathways for genes down-regulated at 4 h in MS300c strain



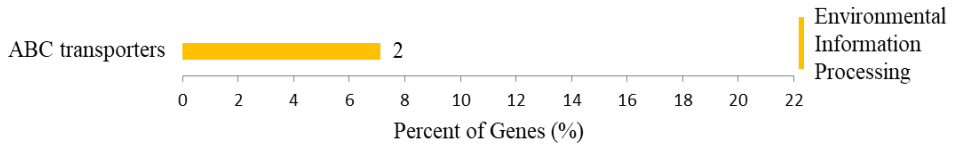
(i) Pathways for genes up-regulated at 4 h in MS300c strain



(j) Pathways for genes down-regulated at 4 h in MS300c- strain



(k) Pathways for genes up-regulated at 4 h in MS300c- strain



(l) Pathways for genes up-regulated at 1 h in MS300c- strain

Figure 4-4. Functional classification of KEGG pathway of assembled unigenes. The KEGG pathways were summarized in four main categories: Cellular Processes; Environmental Information Processing; Genetic Information Processing; Metabolism. The y-axis indicated the name of the KEGG metabolic pathways. The x-axis indicated the percentage of the number of genes annotated under that pathway in the total number of annotated genes.

DE genes

Figure 4-5 shows fold changes of transcript levels of the DE genes found in the 6 significantly commonly over-represented GO terms among four strains. The tendencies of the DE genes shown in Figure 4-5 are thought to be robust since the reproducibility of transcriptional tendencies of each gene was ensured within a gene by triplicate experiments as well as across the genes in the same functional category. Among the 61 DE genes, 24 of them were found to be assembly factors that function in maturation of 40S ribosomal subunits, 26 were found to be assembly factors that function in maturation of 60S subunits in *S. cerevisiae*, and 3 were found to be both 40S and 60S assembly factors (figure 4-5), all of which differentially detected in the four tested strains at 1 and/or 4 h (Table 4-A1). The significant assembly

factors were found to be down-regulated in the strains S288C and S7 at 4 h, but up-regulated in the strain MS300c and MS300c- at 4h. In the S288C strain, all the 47 ribosome assembly factors were significantly down-regulated at 1 h and 4 h. The similar tendency was observed in the S7 strain at 4 h. In the MS300c and MS300c- strains, all the 47 ribosome assembly factors were significantly up-regulated at 4 h. While at 1 h, there were almost no fluctuations for the assembly factors compared with the respective negative controls exposed to 0.1% DMSO only in the MS300c and MS300c- strains. Moreover, several genes of the assembly factors were reported to be important disease related genes. The gene name and related diseases are shown in Table 4-2.

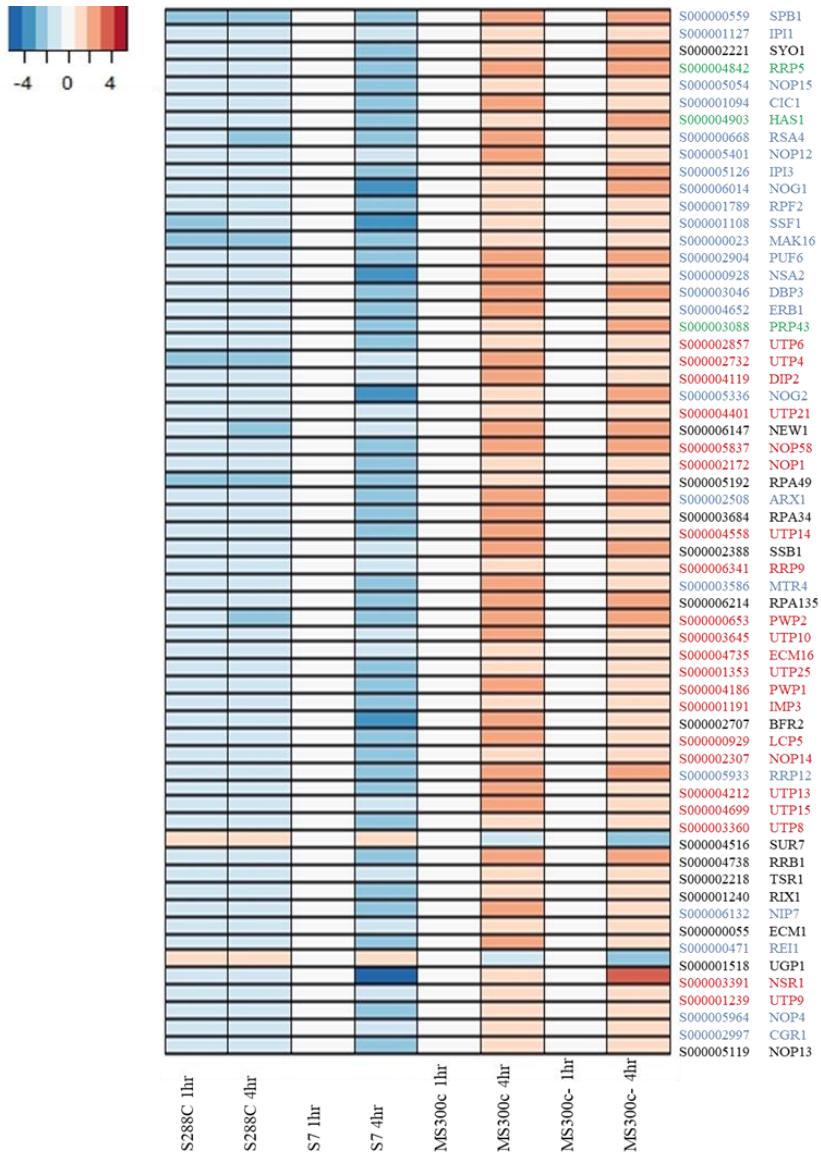


Figure 4-5. Heat map displaying fold changes of transcript levels of the selected DE genes. The genes found in the 6 significantly commonly over-represented GO terms among four strains are shown. The Euclidean distances are shown based on log-transformed fold change values. Genes in red indicate those 40s assembly factors, genes in blue indicate 60s assembly factors, while those in green indicate those both 40s and 60s assembly factors.

Table 4-3. Genetic diseases of ribosome assembly factors.

Gene		Impaired molecular function	Disease	Clinical manifestations	Inheritance and incidence (if known)	Online Mendelian Inheritance in Man (OMIM)	References
human	yeast						
UTP14c	UTP14	maturation of the 18S rRNA of the 40S ribosomal subunit	male infertility	severe oligospermia or azoospermia	unknown	N/A	(Dragon et. al. , 2002, Rohozinski et. al. , 2006)
CIRHIA	UTP4	maturation of the 18S rRNA of the 40S ribosomal subunit	Native American Indian childhood cirrhosis (NAIC)	neonatal jaundice progressing to biliary cirrhosis; lethal by adolescence without liver transplant	autosomal recessive; <100 cases reported	#604901	(Dragon et. al., 2002, Chagnon et. al. , 2002, Prieto and McStay, 2007)
RBM28	NOP4	maturation of the 60S ribosomal subunit	alopecia, neurological defects, and endocrinopathy syndrome (ANE syndrome)	growth retardation, loss of motor ability, mental retardation, skeletal and skin abnormalities, hair loss, central adrenal insufficiency	autosomal recessive	#612079	(Nousbeck et. al. , 2008)

WDR36	UTP21	maturation of the 18S rRNA of the 40S ribosomal subunit	candidate gene for primary open angle glaucoma (POAG)	degeneration of optical nerve leading to blindness	multifactorial	#137760	(Dragon et. al., 2002, Monemi et. al. , 2005)
HCA66	UTP6	maturation of the 18S rRNA of the 40S ribosomal subunit	modifier of neurofibromatosis type 1 (NF1)	mental retardation, craniofacial and connective tissue abnormalities, congenital heart defects, tumor predilection	autosomal dominant	#162200	(Dragon et. al., 2002, Bartelt-Kirbach et. al. , 2009)
IMP3	IMP3	component of the SSU processome, required for pre-18S rRNA processing	candidate gene for Silver-Russell Syndrome (SRS)	pre- and postnatal growth restriction in association with other clinically recognised dysmorphic features such as triangular facies, asymmetry, and fifth finger clinodactyly	autosomal dominant or autosomal recessive	#180860	(Monk et. al. , 2002)

Comparison of killer strain and cured strain

Data analysis was also conducted separately to compare the effect of nitazoxanide on killer strain and cured killer strain. The number of up- and down-regulated DE genes of each strain was shown in Figure 4-6. The number of DE genes at 1 h was much smaller than that at 4 h for two strains. And more DE genes were up-regulated than down-regulated for two time points for two strains (Figure 4-2). As shown in Figure 4-6, there are 333 up-regulated and 92 down-regulated DE genes in common for these two strains combining two time points of 1 h and 4 h. However, there are similar number of unique up-regulated DE genes and much more unique down-regulated DE genes compared to the common ones for both MS300c and MS300c- strains. Over-represented GO terms from MS300c and MS300c- strains were also separately analyzed. Figure 4-7 showed ten most significant GO terms from each main category, including cellular component, molecular function and biological process. For enriched GO terms from up-regulated genes for two strains, they were similar but more molecular functions related GO terms were over-represented in the MS300c strain. However, for the enriched GO terms of down-regulated genes for two strains, they were very different and there is no coincident part between two strains, indicating the change of the attributes of cells by losing the M-dsRNA. Figure 4-4 showed the KEGG pathways analyses results for strains MS300c and MS300c-. For up-regulated genes at 1 h in two strains, the ABC transporters pathways were over-represented in both strains. And for up-regulated genes at 4 h, the over-represented KEGG pathways were similar, while quite different for down-regulated genes at 4 h. More

categories were influenced in strain MS300c- for down-regulated genes at 4 h. MS300c and MS300c- have the same origin but the over-represented GO terms and enriched KEGG pathways were different (Figure 4-4 and Figure 4-7).

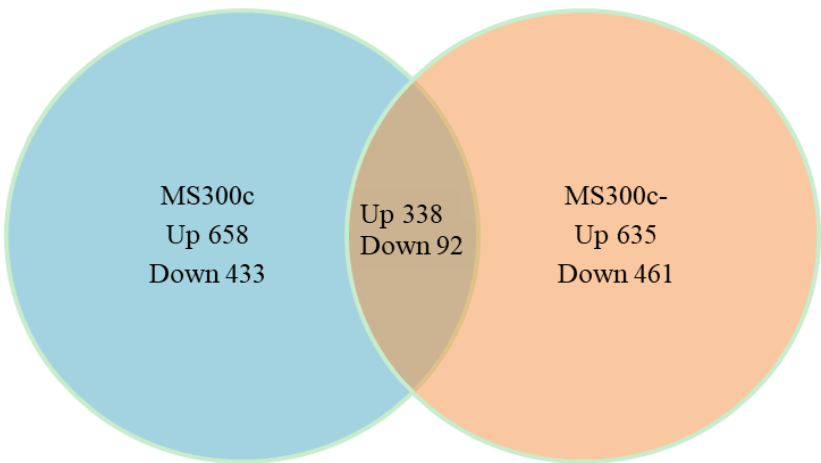
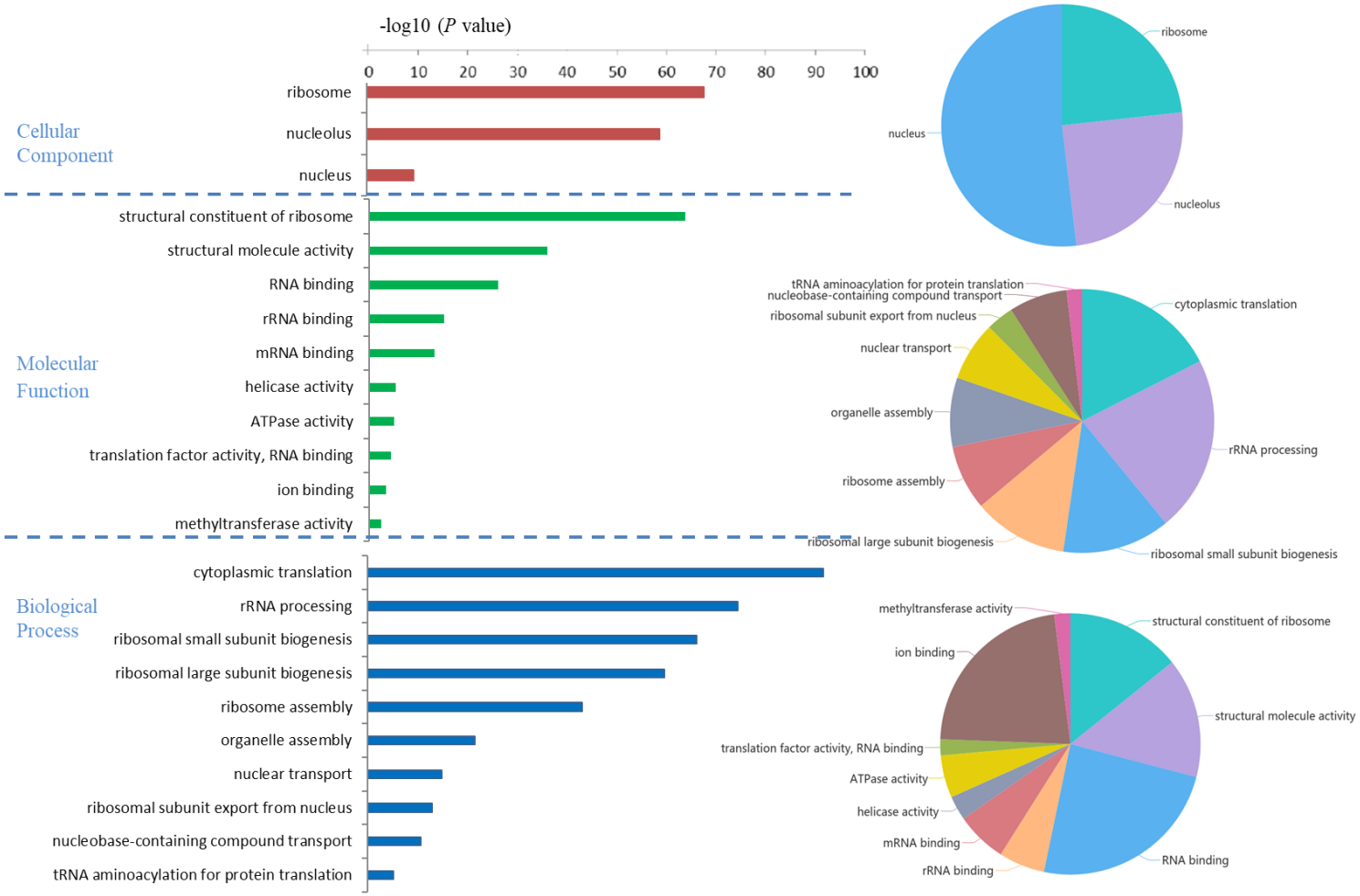
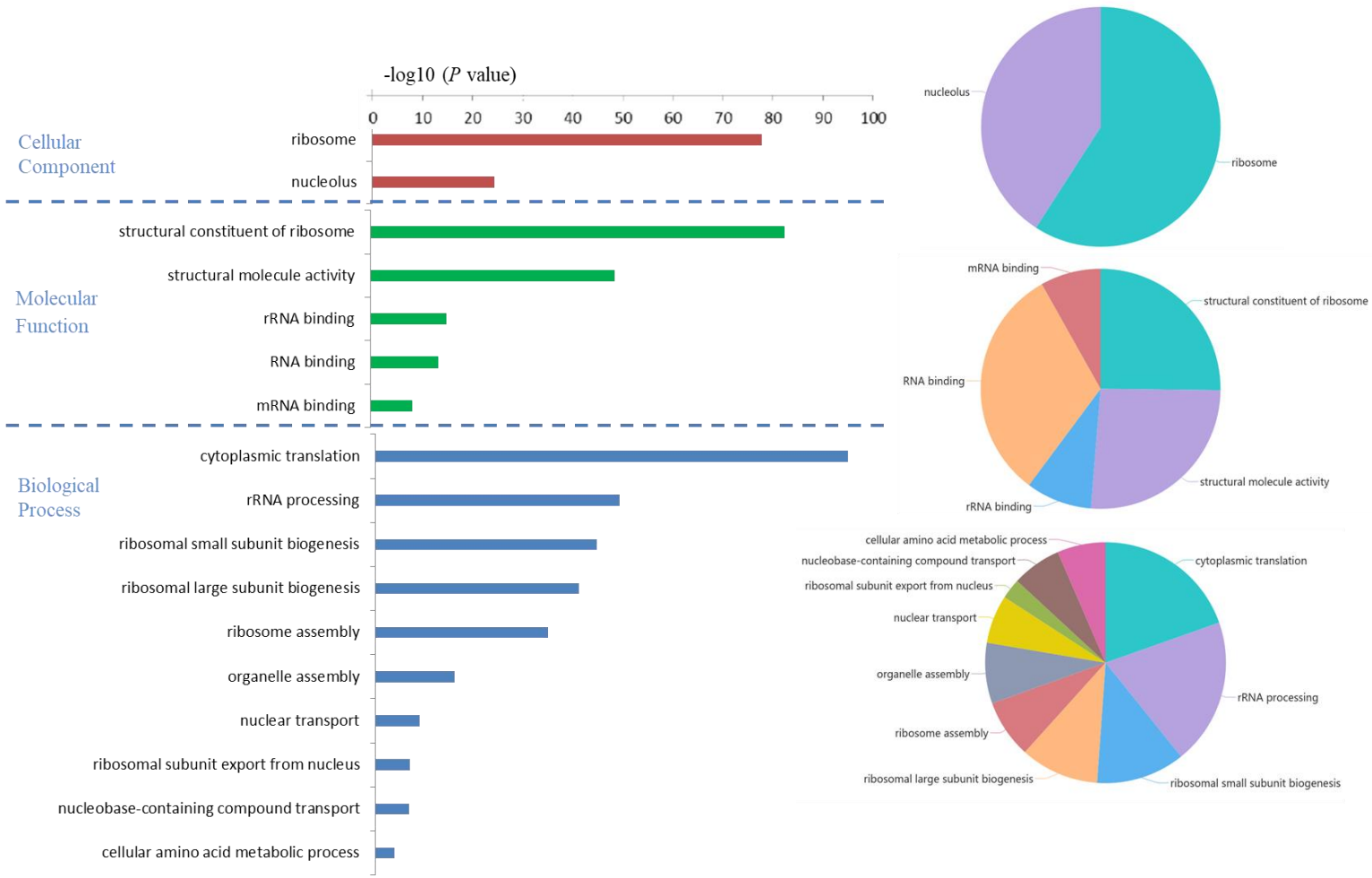


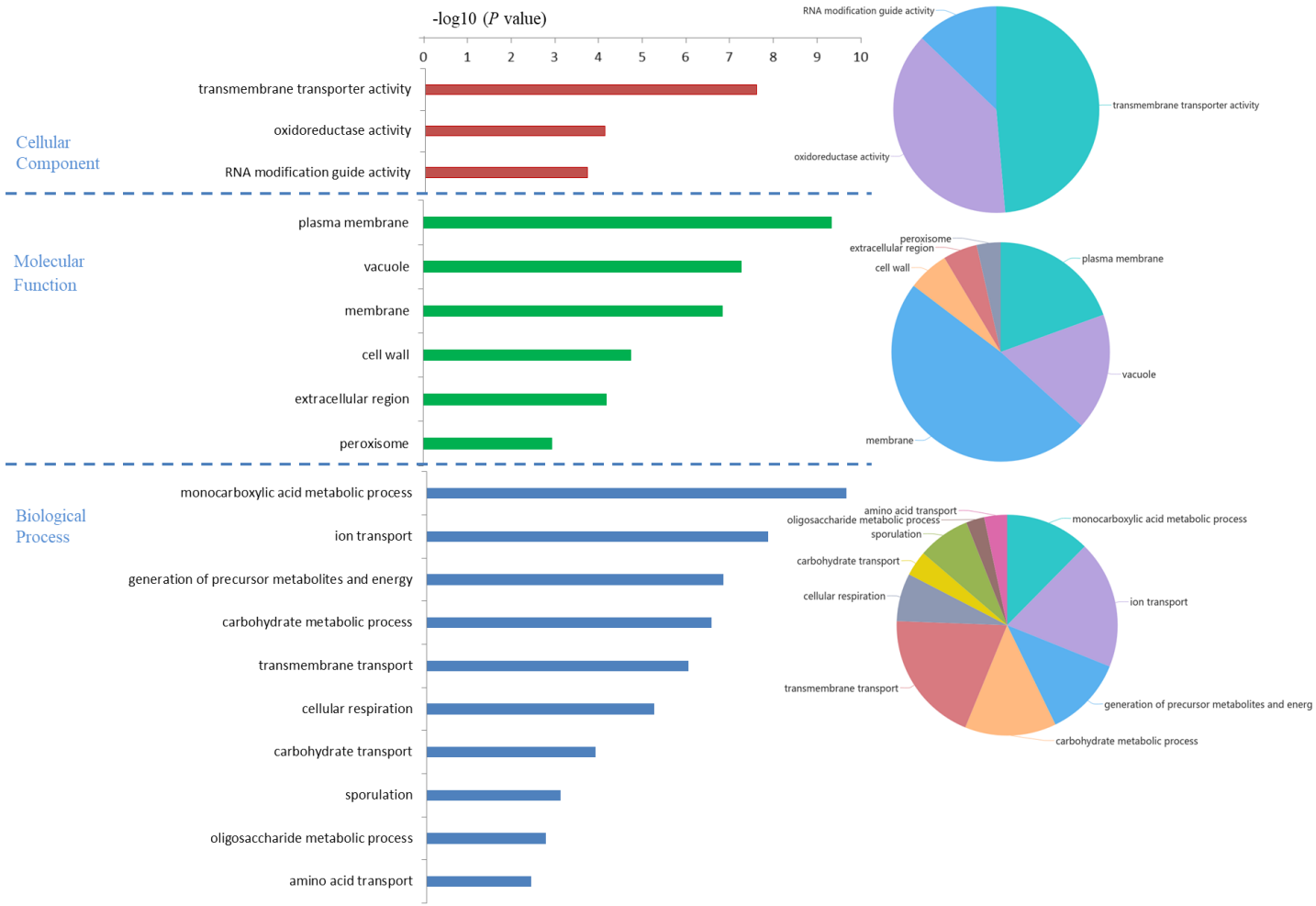
Figure 4-6. Venn diagram showing number of DE genes in MS300c and MS300c- strains.



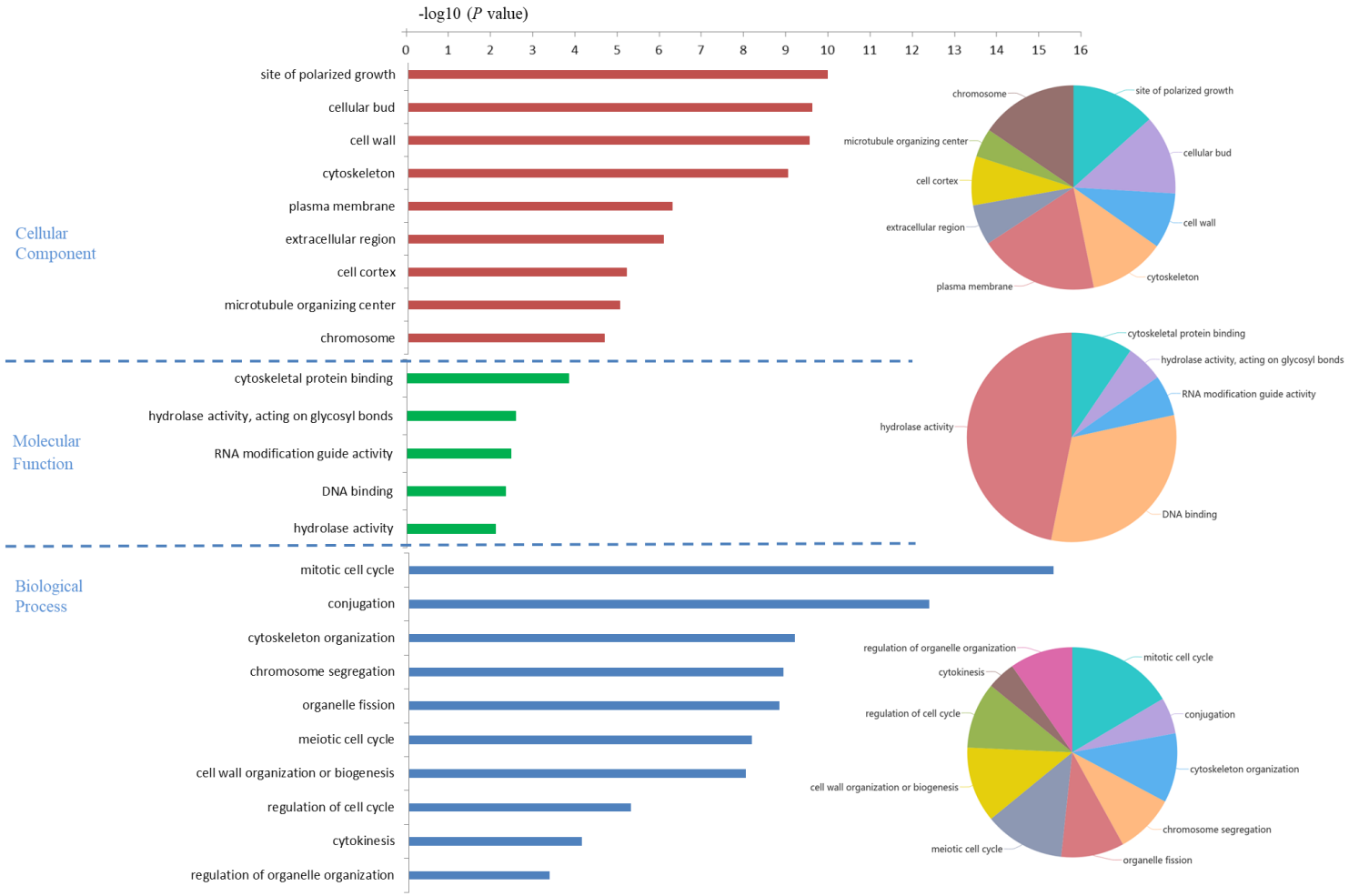
(a) GO analysis of up-regulated genes at 4 h in MS300c strain



(b) GO analysis of up-regulated genes at 4 h in MS300c- strain



(c) GO analysis of down-regulated genes at 4 h in MS300c strain



(d) GO analysis of down-regulated genes at 4 h in MS300c- strain

Figure 4-7. Gene ontology analysis of strains MS300c and MS300c-. Bar graphs show P values of the ten most significant enriched GO terms of each 3 catogories: molecular function, biological process and cellular component. Pie charts show proportion of the genes in different biological functions.

qPCR validation

Six genes were selected from each comparison group for quantitative RT-PCR validation to confirm the changes in gene expression observed by RNA-Seq (Table 4-1). RT-PCR analysis was performed for the genes between treated samples (nitazoxanide exposure) and control samples for two time points (1 h and 4 h). The expression data of genes measured by RNA-Seq and qPCR are shown in Figure 4-8. The results showed obvious positive correlation between qRT-PCR and RNA-Seq transcriptomic data, with correlation coefficient of 0.81, suggesting a good quality of RNA-Seq data (Figure 4-8).

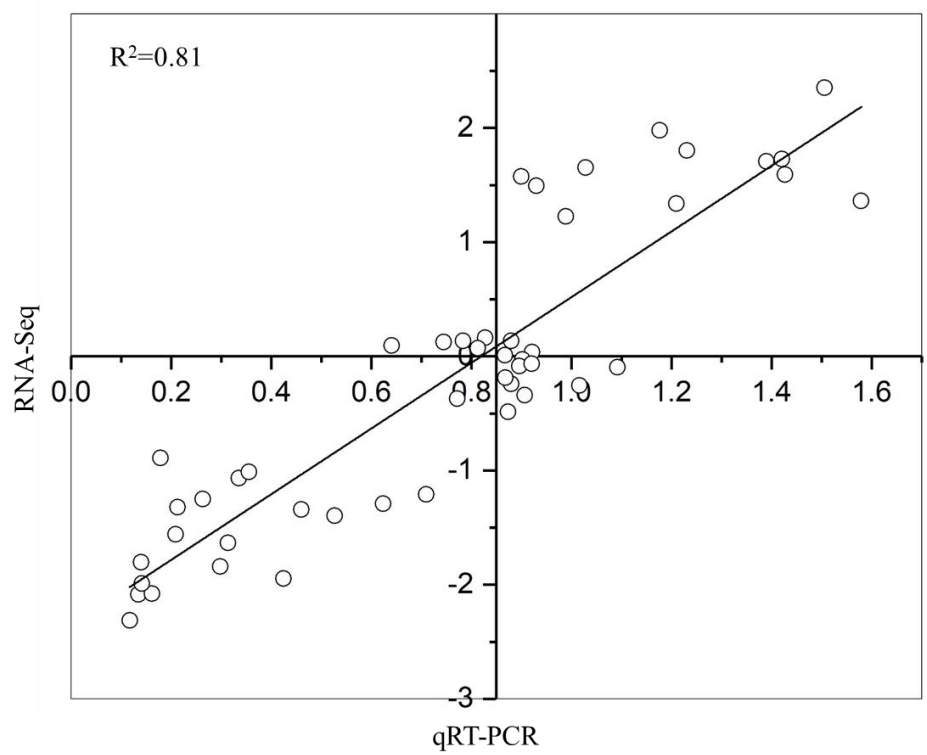


Figure 4-8. Validation of RNA-seq data using qPCR. Fold changes of gene expression detected by RNA-seq were plotted against the data of qPCR. The

reference line indicates the linear relationship between the results of RNA-seq and qPCR.

Discussion

The nitazoxanide exposure concentration we chose, 10 μg/ml, was the peak concentration of the drug in human plasma after receiving a single 500-mg oral dose of nitazoxanide (Broekhuysen et al 2000). This exposure concentration can provide insights into how nitazoxanide impacts on eukaryotic transcriptomes, which is thought to be important when determining elusive mechanisms of action and potential side effects of nitazoxanide on human. On the other side, nitazoxanide cytotoxicity was less than 5% if cells (human umbilical vein endothelial cells) were treated with less than 10 μg/ml for uninfected cells (Ludmila Perelygina 2017). And some other researchers also pointed out that the 50% cytotoxic concentration of nitazoxanide on cells (monkey kidney MA104 cells and human colorectal adenocarcinoma Caco-2 and HT-29 cells) was higher than 50 μg/ml (La Frazia et al 2013).

This RNA-Seq based study found that ribosome biogenesis in *S. cerevisiae* was significantly affected by nitazoxanide exposure (Figure 4-3). It is pointed out that *S. cerevisiae* represents a suitable eukaryotic model organism to study ribosome assembly and related factors due to its easy experimental accessibility (Kressler et al 2010). Ribosomes are the cellular machines that translate the genetic code in mRNA and catalyze protein synthesis in all organisms (Fromont-Racine et al 2003). The production of ribosomes is very closely related to the growth and proliferation of cells,

dysregulation of ribosome assembly has profound consequences on the health of organisms (Woolford & Baserga 2013). Studies have revealed important human genetic diseases of ribosome biogenesis, such as Diamond-Blackfan anemia (DBA) (Choesmel et al 2007), Schwachman-Diamond syndrome (SDS) (Burwick et al 2012) and 5q-syndrome (Galili et al 2009). Researchers also pointed out that pathways and participants in ribosome biogenesis in eukaryotes are proving to be conserved and a complete understanding of ribosome assembly in yeast will enable more rapid understanding of the molecular basis of human disease caused by ribosomopathies (Woolford & Baserga 2013). Thus, the finding of this study that ribosome biogenesis function in *S. cerevisiae* was affected by nitazoxanide exposure is significant for predicting the potential side effects of nitazoxanide treatments for virus infections in human.

Complete loss of ribosome function is expected to be lethal, but dysregulation in ribosome assembly factors can also be the causative agents of several diseases, such as male infertility (Dragon et al 2002, Rohozinski et al 2006), Native American Indian childhood cirrhosis (NAIC) (Chagnon et al 2002, Dragon et al 2002, Prieto & McStay 2007), alopecia, neurological defects, and endocrinopathy syndrome (ANE syndrome) (Nousbeck et al 2008). Ribosomes are composed of two ribonucleoprotein subunits, including the small, 40S subunit (SSU) and the large, 60S subunit (LSU). There are more than 170 different assembly factors participating in the formation of ribosomes in yeast, and more than 70 of them are 40S ribosomal subunits assembly factors, and approximately 90 of them are 60S ribosomal subunits assembly factors (Fromont-Racine et al 2003, Woolford

& Baserga 2013). In this study, there are totally 2378 DE genes detected among four strains, indicating the dramatic drug effect by nitazoxanide in *S. cerevisiae* strains. The DE genes detected in this study include 24 40S ribosomal subunits coding genes and 26 60S subunits coding genes, such as UTP14, UTP4, NOP4, UTP21, UTP6, and IMP3, which are the causative agents of several genetic diseases (Table 4-3). This finding in turn, also confirmed the previous conclusion that ribosome biogenesis function was affected by nitazoxanide exposure and may lead to related diseases in humans treated by nitazoxanide for virus infections. Moreover, the assembly factors coding genes detected in our study were found to show a clear different time trend in different strains. They were down-regulated in the strains S288C and S7 at 4 h, but up-regulated in the strain MS300c and MS300c- at 4h. Our results suggest that these assembly factors coding genes might be up regulated first and then down regulated. The trend seems reasonable because we found the growth speed of S288C and S7 was faster than the other two strains, including MS300c and MS300c-. However, the detailed mechanisms are not clear now. Nitazoxanide exposure time also influenced significantly and the degree of effect at two time points in different strains are different (Figure 4-1 and Figure 4-2). For instance, in the strains of S7, MS300c and MS300c-, there are much more DE genes, both up- and down-regulated genes at 4 h than that at 1 h. While in strain S288C, there are considerable DE genes in 1 h compared to other strains, indicating the effect of nitazoxanide was more rapidly expressed in the strain S288C.

Generally, the mechanism of nitazoxanide against hepatitis C virus includes the activation of protein kinase, which results in phosphorylation of eukaryotic initiation factor 2 alpha (eIF2α), a gene known to block viral replication (Elazar et al 2009, Rossignol et al 2008). The mechanism against influenza virus is that nitazoxanide blocks the maturation of the viral hemagglutinin at the post-translational stage (Rossignol et al 2009). For rotavirus, nitazoxanide can inhibit the maturation of viral protein 7 (VP7), which constitutes the outer portion of virion. The specific mechanisms against other viruses are not well-known. Overall, studies of the mechanisms of action of nitazoxanide against viruses have shown that the drug is attributed to interference with host-regulated pathways involved in viral replication, rather than a virus-targeted mechanism (Belardo et al 2015, Keeffe & Rossignol 2009). Thus, it is more important to study the effect of nitazoxanide on the virus hosts to explore the mechanisms of nitazoxanide. KEGG pathway is a collection of manually drawn pathway maps representing our knowledge on the molecular interaction, reaction and relation networks for metabolism, genetic information processing, environmental information processing, cellular processes, human diseases and drug development (Kanehisa & Goto 2000). The results of KEGG pathway analysis in this study showed that the DE genes related to total 4 main categories, including genetic information processing, metabolism, cellular processes and environmental information processing. Specifically, among the commonly detected pathways across different strains, two of the largest multi-protein complexes- Utp A and Utp B in the pathways of

ribosome biogenesis, were found to be largely affected by nitazoxanide exposure. Utp A is a protein complex composed of Utp4, Utp8, Utp9, Utp10, Utp15, Pol5 and Nan1. Utp B is a six-protein complex consisting of Utp6, Utp13, Utp18, Utp21, Dip2 and Pwp2 (Poll et al 2014). In this study, among these 13 proteins, 10 protein coding genes were found to be significantly differentially expressed in four strains, 2 protein coding genes (Utp 18 and Nan1) were found to be differentially expressed in three strains with the exception of Pol5, who didn't show differential expression in our study. It has been reported that Utp A initiates eukaryotic ribosome biogenesis and contains a large composite RNA-binding site (Barandun et al 2018). Utp B is an essential component of the 90S precursor of small ribosomal subunit and it provides a binding platform for early pre-ribosomal intermediates such as an RNA duplex formed by the 5′ ETS and U3 snoRNA as well as the 3′ boundary of the 18S rRNA (Hunziker et al 2016). Both complexes therefore act as vital RNA chaperones to initiate eukaryotic ribosome assembly and normal production of protein. Previous studies have mentioned nitazoxanide affected some specific proteins to influence the viral production. Our study suggests that nitazoxanide affects ribosome biogenesis mainly through affecting UtpA and UtpB complexes as an attempt to anatagonize viral replication and spread. This also indicates that the barrier to development of antiviral resistance is significantly higher for nitazoxanide than for drugs directly targeting a viral function. Besides, interestingly, the pathway biosynthesis of antibiotics was also commonly detected in four strains, which may indicate nitazoxanide can trigger the yeast cell to produce antibiotics to inhibit the virus replication.

Besides, data analysis was also conducted to compare the *S. cerevisiae* killer strain MS300c and its cured strain MS300c-. Interdelta PCR confirmed that the cure strain MS300c- was truly originated from killer strain MS300c excluding the possibility of contamination (Figure 2-3). The numbers of DE genes detected in two strains are similar for both up- and down-regulated DE genes combining two time points. But half of the up-regulated and three quarters of the down regulated DE genes are unique (Figure 4-6), indicating the drug effect are different on the two strains. GO term enrichment analysis and KEGG pathways analysis also revealed that the reactions of the two strains are distinct especially for down-regulated genes (Figure 4-7 and Figure 4-4). Since the killer strain and cured strain have the same origin, the difference between them might attribute to the lost of the M-dsRNA.

This study utilized the *S. cerevisiae* as a model organism to characterize the effects of the antiviral drugs, which may predict the effects of the antiviral drugs on human and other eukaryotes. However, admittedly, *S. cerevisiae* is among the best model organisms, a part of its genes (around 60%) still have no experimentally determined function, which may produce some variances when comparing with human genomes (Mohammadi et. al. , 2015). While on the other hand, it's very likely that a newly discovered human gene will have a yeast homolog with at least some common functional information, since *S. cerevisiae* still has large undiscovered similarities with humans.

This chapter reported that nitazoxanide affected ribosome biogenesis functions in yeast, which might be one of the reference data when considering side effects and underlying mechanism in human treated for viral infections by nitazoxanide, currently in Phase II/III clinical trials.

CHAPTER V.

Conclusions

Summary and Conclusions

This RNA-Seq-based study provides insights into how ribavirin and nitazoxanide impact on eukaryotic transcriptomes, which is thought to be important when determining elusive mechanisms of action and side effects of them. Particularly, this study pointed out that the relationship between reported side effects of ribavirin and the dysregulation of small non-coding RNAs detected in this research should be scrutinized. For nitazoxanide, this study predicted the potential side effects of nitazoxanide related to the dysregulation of ribosome biogenesis, which is significant since nitazoxanide is under clinical test now and potentially will be used as an antiviral drug in the future. In addition, this study also developed new and efficient low-cost method for testing antiviral efficiency and safety, which can be further developed into a high throughput screening protocol for searching antivirals. Specifically, the thesis contained three research chapters including testing the effectiveness of ribavirin and nitazoxanide on *S. cerevisiae* killer strain (Chapter II); Utilizing RNA-Seq to characterize effects of ribavirin on whole transcriptomes of *S. cerevisiae* strains containing dsRNA virus-like particles (Chapter III); Utilizing RNA-Seq to characterize effects of nitazoxanide on whole transcriptomes of *S. cerevisiae* strains containing dsRNA virus-like particles and *S. cerevisiae* cured strains (Chapter IV).

In the first research chapter (Chapter II), to provide basic evidence and background for the following two chapters' research, the effectiveness of ribavirin and nitazoxanide on *S. cerevisiae* killer strain was tested. Antiviral

drugs ribavirin and nitazoxanide were used to cure the *S. cerevisiae* killer strain respectively. The curing results were confirmed by halo assay and molecular methods. As shown in Figure 2-1 and Figure 2-2, both ribavirin and nitazoxanide are effective to remove the M dsRNA from the *S. cerevisiae* killer strain and the killer strain lost their killing traits. This study not only developed new approaches to cure the *S. cerevisiae* killer strain, but also confirmed the effectiveness of these two antiviral drugs. Therefore, it provide background information for the following two chapters, which were going to evaluate the effects of antiviral drugs on the cells *of S. cerevisiae*.

In Chapter III, based on chapter II, ribavirin was firstly used to study the effects on whole transcriptomes of *S. cerevisiae* utilizing RNA-Seq techniques. Three strains were chose as tested strains with different genotypes. Through RNA-Seq data analysis, I observed the accumulation followed by reduction of small nuclear (sn)RNAs and small nucleolar (sno)RNAs in *Saccharomyces cerevisiae* exposed to ribavirin. The three strains reported to contain dsRNA virus-like particle(s) were exposed to 100 μM of ribavirin, and snRNAs and snoRNAs from a total of 31 *snR* genes were differentially detected between the samples exposed to ribavirin and the respective negative controls by mRNA-Seq. Our results suggest polyadenylated snRNAs and snoRNAs accumulated at 1 h but reduced to the sub-basal levels at 4 h of ribavirin exposure. The tendency was reproducible across the three tested strains. Our study showed ribavirin affected snRNAs and snoRNAs in yeast. Ribavirin is an antiviral drug that is used to treat a wide range of human viral infections. However, the side effects are reported, and the mechanisms on eukaryotic cells are still largely

unknown. There may be a need to scrutinize the relationships between the side effects and such ncRNAs in humans who are treated with ribavirin.

In Chapter IV, similar study design was utilized as Chapter III. But the cured strain of *S. cerevisiae* killer strain was also tested. RNA-Seq was utilized to characterize the effects of nitazoxanide on the whole transcriptomes of *S. cerevisiae* containing dsRNA virus-like particles and cured strains. Nitazoxanide exposure experiment was first conducted on four strains and total RNA was extracted from each library before proceeding to the RNA-Seq experiment. This RNA-Seq based study found that ribosome biogenesis related functions in *S. cerevisiae* were significantly affected by nitazoxanide. The dysfunctions of ribosome are known to be related to several human diseases, thus the finding of this study is very important. It provides insightful hints to the potential side effects of the utilization of nitazoxanide. Our study found that the enriched KEGG pathways mainly belongs to metabolism such as metabolic pathways and biosynthesis of secondary metabolites, genetic information processing such as ribosome biosynthesis in eukaryotes and ribosome, which may reflect *S. cerevisiae* cells' response to nitazoxanide exposure as an attempt to antagonize viral replication and spread. The RT-PCR validation experiment also confirmed the good quality of the RNA-Seq transcriptomic data.

Future Studies

This study is the first research to characterize the effects of the antiviral drugs using *S. cerevisiae* as a model organism by RNA-Seq so far. If similar datasets become available in the future, comparison studies with these

datasets can be conducted to look for the common and difference points of antiviral drugs' effects in different virus hosts. For future studies, similar methodology can be further developed and utilized to screen other important drugs with reported side effects or upcoming drugs to seek for the underlying reasons of side effects or potential side effects. Besides, since one of the limitations of this study is that only one concentration was tested for each drug, a series of different concentrations can be tested in the future, such as environmental related lower concentrations. In addtion, since *S. cerevisiae* is the simplest eukaryote being utilized as a model organism in this study, other more complicated cells, such as animal or human cells can be used to characterize the effects of antiviral drugs in the future.

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APPENDICES

Table 3-A1. FPKM values and statistical significance of the differentially expressed genes of the *S. cerevisiae* strains.

Gene	Gene short name	ATCC 204508 (S288C)						ATCC 44828 (S7)						ATCC 201204 (MS300c)					
		1 h			4 h			1 h			4 h			1 h			4 h		
		B	E	Sig	B	E	Sig	B	E	Sig	B	E	Sig	B	E	Sig	B	E	Sig
S000000023	MAK16	34.6	20.3	*	30.5	31.9		24.4	19.2		16.3	17.8		115.2	88.0		72.9	71.2	
S000000135	URA7	29.5	15.2	*	22.1	18.3		19.5	15.6		10.1	9.8		105.2	75.1		82.2	69.2	
S000000270	NRG2	14.1	27.6	*	8.1	11.4		22.0	13.2		18.4	16.1		32.4	21.1		22.8	18.8	
S000000302	MMS4	11.5	27.8	*	8.7	9.4		30.7	29.6		31.1	34.3		11.7	13.2		16.7	17.5	
S000000488	YBR284W	6.8	14.4	*	3.7	4.3		31.3	26.8		31.4	27.5		4.5	4.9		6.4	6.5	
S000000613	PET18	6.3	38.8	*	6.6	6.6		15.4	10.5		14.9	13.3		4.2	5.6		6.5	5.2	
S000000858	FCY2	142.0	69.8	*	133.0	104.2		52.2	71.8		43.4	42.6		252.1	189.9		339.6	237.6	
S000001134	HXT4	130.9	74.9		7.4	16.7	*	86.4	61.1		53.6	55.4		333.4	505.7		435.1	442.6	
S000001147	YPT35	7.0	17.5	*	7.6	7.1		20.4	21.6		17.7	20.3		10.7	12.6		12.1	11.1	
S000001168	ANS1	11.6	7.8		14.9	9.9		1.4	1.1		3.8	2.7		52.0	21.4	*	35.2	24.5	
S000001379	PRM5	116.9	105.8		41.8	45.9		86.8	51.4	*	48.1	46.5		145.4	140.3		140.9	125.6	
S000001381	RPI1	27.4	36.8		22.7	18.2		11.3	9.8		11.6	8.0		21.1	12.3	*	24.6	20.0	
S000001385	SIM1	114.9	91.2		67.4	68.5		66.0	35.9	*	31.4	30.8		174.1	139.8		301.1	295.3	
S000001527	YKL044W	25.0	60.9	*	13.9	17.5		32.8	40.9		31.7	33.6		65.3	48.5		25.9	26.0	
S000001700	JEN1	1215	1059		463.0	576.4		1080	1115		991.2	974.7		33.5	59.8	*	77.8	81.8	
S000001721	PRY2	400.3	235.3		126.8	138.5		194.9	71.6	*	46.5	45.9		1331	848.5		1549.7	1444.8	
S000001841	DAK2	4.3	6.9		4.4	4.1		18.3	9.5	*	12.5	10.1		13.3	9.6		11.7	12.9	
S000001956	CWP2	12864	11894		10135	11628		3335	1769	*	1426	1569		17925	13665		19398	19158	
S000002836	BNA7	13.3	23.9	*	11.9	13.6		50.1	45.4		37.5	44.8		17.9	18.9		14.8	16.0	
S000002942	FIT1	2.9	2.8		2.7	2.4		3.8	1.8	*	2.5	2.4		1.0	0.8		0.9	0.9	
S000003267	YGR035C	14.0	30.1	*	8.9	10.2		6.3	5.8		7.4	5.0		52.9	48.9		28.0	23.4	
S000003391	NSR1	148.1	75.7	*	138.4	113.9		114.8	64.0	*	70.1	55.9		416.5	277.7		292.9	227.2	
S000003468	SPG1	276.5	502.5	*	150.7	170.5		876.8	1207		1029	1024		17.0	27.9		42.4	69.1	
S000003524	MAL12	3.2	6.4	*	4.4	4.7		44.6	45.6		33.2	34.8		8.4	10.1		8.8	9.8	
S000003624	ARG3	166.6	158.8		181.6	184.4		47.9	26.9	*	37.2	30.3		164.2	182.8		160.4	141.8	
S000003694	CIS3	659.6	602.4		323.7	360.0		308.1	157.7	*	114.8	117.0		1529	1159.7		1444.2	1275.4	
S000004032	YLR042C	27.8	14.3		7.8	10.1		26.9	13.8	*	14.6	14.6		273.4	186.5		334.1	265.6	
S000004787	SIP18	322.4	694.2	*	350.0	406.7		147.0	197.9		180.3	171.7		37.3	23.6		90.4	105.4	
S000004942	ERR3	3.0	6.0	*	1.8	2.3		11.2	14.3		8.5	10.8		0.9	1.1		2.0	1.9	
S000004953	ASI3	30.3	87.4	*	24.4	28.4		49.4	50.4		50.8	48.1		47.9	47.6		39.8	42.7	
S000004954	IDP3	27.5	48.7	*	31.4	35.1		73.8	72.2		86.7	73.3		11.6	13.8		19.6	20.7	
S000005056	DBP2	85.2	27.6	*	54.8	35.4		25.6	27.7		21.1	21.2		203.1	129.6		206.1	148.4	
S000005070	SPC98	6.7	11.7	*	5.8	8.0		16.7	12.7		10.5	11.5		11.0	11.7		14.7	16.0	
S000005085	AAH1	30.7	20.8		21.2	19.5		21.1	19.0		24.2	16.9		121.6	67.1	*	64.1	56.6	
S000005192	RPA49	36.2	21.2	*	25.3	25.6		27.4	23.0		16.4	15.0		156.3	125.4		97.0	84.6	
S000005233	PCL1	10.1	5.0	*	17.4	23.7		16.6	8.8		6.3	6.8		32.8	23.3		82.8	75.3	
S000005244	TOS6	163.7	68.8	*	48.6	57.8		75.4	49.2		47.3	53.7		179.8	103.5		414.4	430.6	
S000005327	AGA1	30.1	24.4		9.9	11.7		29.8	15.6	*	12.6	13.2		117.2	76.9		23.9	22.9	
S000005349	YNR066C	10.2	20.1	*	8.9	8.4		9.8	10.4		10.6	9.9		7.5	8.3		6.3	7.5	
S000005461	IZH4	28.7	20.7		24.0	17.7		11.1	8.8		9.2	8.2		166.7	83.6	*	146.8	101.1	
S000005554	CIN5	17.9	28.7		10.3	12.9		37.3	13.2	*	14.5	17.9		86.3	75.4		64.3	64.3	

S000005740	SPR2	0.8	2.8	*	0.8	1.3		4.4	2.7		2.3	3.6		1.0	0.9		1.3	2.0	
S000005773	SRL1	305.6	281.2		164.0	186.3		360.4	197.9	*	177.7	192.4		445.4	333.6		1341.3	1263.1	
S000005823	TIM18	62.4	118.1	*	74.3	74.3		90.5	88.0		71.9	77.5		72.4	72.7		80.1	79.9	
S000005824	MUM3	10.3	43.1	*	4.3	4.0		37.9	23.7		21.9	26.8		6.8	6.1		5.4	6.2	
S000005842	SFG1	7.4	9.1		5.1	9.5	*	12.5	9.9		8.4	9.3		14.2	13.1		23.0	20.1	
S000005937	SWI1	12.8	26.0	*	6.9	7.6		24.6	10.7	*	13.0	12.4		4.9	3.7		10.7	11.0	
S000006084	SVS1	100.0	42.8	*	27.2	30.7		81.3	36.3	*	25.2	25.9		345.5	217.8		659.0	604.1	
S000006144	GRE1	73.0	145.0	*	94.1	132.9		106.0	110.5		97.0	96.5		34.4	24.1		60.2	57.4	
S000006442	snR51	647.9	275.2		0.0	351.0		0.0	0.0		742.0	0.0	*	0.0	0.0		0.0	301.0	
S000006454	snR63	145.3	316.1	*	228.8	86.4	*	75.4	120.6		174.4	102.2		50.9	66.8		43.1	31.8	
S000006478	LSR1	156.0	335.5		301.5	132.9	*	67.4	84.0		145.2	113.3		83.7	92.6		86.8	56.1	
S000006490	RPR1	12.0	29.2	*	19.8	10.6		16.7	20.0		19.4	17.8		22.9	24.3		15.6	10.1	
S000006491	SCR1	357.9	958.1	*	793.0	296.6	*	152.2	336.1	*	458.8	340.3		211.9	301.3		254.0	104.8	*
S000006492	snR3	67.1	222.9	*	122.1	52.1	*	37.6	51.3		60.1	55.6		31.1	38.2		40.9	18.2	
S000006493	snR4	627.1	1100	*	1096	668.8		355.2	557.6		707.9	576.5		242.0	295.5		346.5	248.0	
S000006497	snR8	50.4	115.5	*	90.8	66.9		26.8	51.5		58.1	63.5		44.6	43.2		38.3	22.1	
S000006500	snR34	271.2	721.7	*	545.1	231.3	*	112.9	149.7		316.6	230.9		106.7	111.9		101.7	44.2	*
S000006501	snR37	230.2	634.7	*	630.3	214.6	*	66.4	119.0	*	248.3	133.3	*	103.3	104.8		106.3	51.0	*
S000006502	snR42	52.9	130.0	*	99.9	68.6		77.2	74.1		96.6	83.6		35.9	39.8		56.1	54.5	
S000006503	snR43	36.9	105.8	*	68.4	38.1		20.5	23.5		31.8	29.8		37.6	43.8		34.3	26.8	
S000006505	snR45	364.4	1064	*	844.2	351.7	*	135.4	239.1		368.5	288.9		160.9	136.9		190.5	93.0	
S000006506	snR46	151.1	363.0	*	254.5	141.0		78.7	108.4		143.9	128.5		48.1	61.1		63.5	23.7	*
S000006508	snR128	150.3	703.3	*	554.2	189.6		164.1	235.7		231.1	236.7		335.2	296.2		231.9	63.7	
S000006509	snR190	1148	3511	*	2454	1159	*	760.4	1456	*	1486	1416		348.6	366.8		550.1	201.8	*
S000007225	YLR035C-A	0.9	1.0		1.6	0.6		4.1	0.4	*	0.1	2.5	*	2.7	7.2	*	7.9	4.7	
S000007252	YOL013W-B	2.9	5.4		2.6	1.5		5.1	10.5		1.1	8.7		2.2	0.0		4.2	0.0	*
S000007268	ATP6	9.4	26.1	*	27.1	13.9	*	2.9	2.5		7.1	4.2		0.0	0.0		0.0	0.0	
S000007270	COB	19.4	42.7	*	42.2	18.1	*	8.1	12.3		23.3	12.2		0.0	0.0		0.0	0.0	
S000007274	OLI1	198.3	516.6	*	405.9	197.7	*	51.1	84.4		133.4	91.2		0.0	0.0		0.0	0.0	
S000007281	COX2	33.8	92.4	*	96.5	38.3	*	19.7	31.0		60.0	39.1		0.0	0.0		0.0	0.0	
S000007283	COX3	26.6	69.9	*	57.8	28.0	*	10.7	16.2		27.3	18.1		0.0	0.0		0.0	0.0	
S000007287	15S_RRNA	170.2	493.2	*	499.3	236.5	*	82.6	124.3		222.4	137.1		0.0	0.0		0.0	0.0	
S000007291	snR5	94.9	246.1	*	164.8	124.2		50.1	79.4		81.6	101.7		53.9	54.1		58.7	47.3	
S000007293	snR11	230.7	410.2	*	306.0	234.8		343.4	368.2		392.7	370.7		123.3	136.9		148.3	134.5	
S000007294	snR17a	75.1	215.7	*	155.9	100.2		66.0	91.9		110.9	132.8		60.4	65.7		60.5	42.3	
S000007295	snR19	239.2	520.3	*	425.4	197.2	*	78.1	104.6		178.5	127.5		71.7	86.7		94.9	41.6	*
S000007297	snR32	105.4	422.4	*	309.7	162.1	*	54.3	68.7		87.5	101.9		63.7	67.3		78.0	57.5	
S000007299	snR35	262.1	733.3	*	589.9	300.6	*	124.2	257.4	*	340.5	243.8		140.6	124.3		144.6	85.7	
S000007300	snR36	79.6	305.8	*	229.5	88.7	*	50.8	77.0		115.6	70.0		50.6	80.1		63.0	46.6	
S000007305	snR41	599.9	0.0		2306	0.0	*	0.0	631.8		0.0	785.9		924.2	0.0		0.0	1221.4	
S000007310	snR76	108.5	285.1		0.0	64.9		545.2	298.4		479.7	160.3		0.0	544.0	*	0.0	0.0	
S000007314	snR189	117.3	415.9	*	230.4	110.7	*	50.3	91.7		103.7	97.2		64.9	71.2		58.7	32.8	
S000007352	YOR142W-B	0.2	0.3		0.1	0.2		0.3	0.5		0.3	0.2		1.0	0.8		2.6	0.9	*
S000007377	YLR256W-	2.9	2.0		1.6	1.8		1.1	0.6		3.2	9.2	*	7.2	33.7	*	4.1	18.0	*

	A																	
S000007381	YML045W-A	5.0	5.0		4.1	5.2		4.6	2.2	*	2.3	3.9		7.9	7.0		3.8	3.5	
S000007393	YDR210W-B	0.5	0.5		0.5	0.9		4.8	1.9	*	0.6	0.2		14.6	4.8	*	26.9	27.9	
S000007397	YDR261W-B	1.5	1.4		1.0	1.4		16.5	10.9		7.2	7.7		13.8	3.7	*	22.9	23.5	
S000007401	YDR365W-B	0.8	0.9		1.3	0.5	*	0.4	0.5		0.3	0.3		6.3	5.5		4.7	4.8	
S000007436	NME1	55.3	168.8	*	126.0	47.5	*	37.5	39.9		78.6	55.8		48.0	42.3		37.0	26.5	
S000007441	snR17b	13.0	37.1	*	23.1	12.2	*	16.4	27.4		36.4	32.0		16.9	15.5		14.1	10.3	
S000007460	snR49	414.1	990.9	*	794.4	353.3	*	224.0	279.7		514.0	165.0	*	147.7	137.2		164.3	48.2	*
S000007499	snR10	220.0	542.1	*	386.0	196.6	*	109.5	148.8		260.3	152.8		90.6	101.5		117.5	75.7	
S000028466	snR84	47.5	90.8	*	64.7	39.4		43.0	35.4		58.4	45.6		44.2	40.2		36.7	28.2	
S000028467	snR82	88.1	187.2	*	218.8	106.9	*	66.9	97.9		120.5	99.6		72.7	75.5		63.4	62.8	
S000028468	snR83	139.0	381.9	*	248.3	117.4	*	109.7	133.8		198.4	152.1		58.3	68.2		101.7	84.1	
S000028573	YML054C-A	9.9	2.4		2.7	8.5		19.3	0.0	*	16.1	6.1		2.8	2.5		7.1	4.8	
S000028579	DGR1	3.2	7.9		10.1	6.5		7.7	23.8		15.1	0.0	*	0.0	0.0		4.4	3.7	
S000028581	YOR011W-A	3.2	7.1		2.4	1.8		3.3	0.0	*	2.2	2.7		0.0	0.0		2.3	0.8	
S000028606	YBR298C-A	0.0	2.6	*	0.8	0.0		0.0	0.0		0.0	0.0		0.0	0.0		0.0	0.8	
S000028635	YGL188C-A	6.1	17.8		4.3	4.2		18.5	59.9		13.1	7.4		20.4	26.1		25.6	0.0	*
S000028691	YMR001C-A	1.0	0.6		0.0	2.8	*	2.5	1.4		0.0	0.9		4.7	2.8		7.1	5.7	
S000028712	YOR161C-C	0.0	13.4	*	0.0	0.0		9.4	16.6		18.2	29.0		0.0	8.6		0.0	15.8	
S000028830	YHR007C-A	44.1	57.4		17.3	18.6		60.3	19.4	*	28.8	31.7		34.0	26.7		78.0	88.9	
S000028838	YIR021W-A	1.5	0.0		1.5	1.6		3.0	2.1		0.7	3.0		0.8	0.0		3.6	0.0	*
S000028848	YMR175W-A	0.9	3.3		3.5	2.2		4.2	1.4		4.7	4.2		1.1	2.4		0.0	4.6	*
S000028851	YNL146C-A	3.0	8.3		1.3	0.0		16.0	0.0	*	5.9	4.5		1.1	0.0		0.0	1.0	
S000029023	RPM1	5.2	17.9	*	14.3	8.6		0.0	0.2		0.4	0.3		0.0	0.0		0.0	0.0	
S000081376	snR85	42.4	134.2	*	77.5	49.5		16.2	34.2		27.3	26.5		12.3	13.8		21.4	14.0	

B: Blank; E: Exposed

Table 3-A2. Full Gene Ontology terms based on up-regulated differentially expressed genes at 1 h in the S288C strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
0030558	RNA pseudouridylation guide activity	3.74E-31	19	60	28	6381
0030559	rRNA pseudouridylation guide activity	3.74E-31	19	60	28	6381
0005732	small nucleolar ribonucleoprotein complex	4.35E-31	27	60	106	6381
0000944	base pairing with rRNA	2.24E-30	24	60	73	6381
0031429	box H/ACA snoRNP complex	1.43E-29	19	60	33	6381
0072588	box H/ACA RNP complex	1.43E-29	19	60	33	6381
0031118	rRNA pseudouridine synthesis	2.77E-29	19	60	34	6381
0005697	telomerase holoenzyme complex	2.27E-28	19	60	37	6381
0044452	nucleolar part	2.43E-27	27	60	148	6381
0030555	RNA modification guide activity	2.43E-27	22	60	71	6381
0030556	rRNA modification guide activity	2.43E-27	22	60	71	6381
0001522	pseudouridine synthesis	1.98E-26	19	60	45	6381
0019843	rRNA binding	2.57E-23	24	60	140	6381
0000154	rRNA modification	8.02E-23	21	60	93	6381
0005730	nucleolus	1.08E-16	27	60	366	6381
0009451	RNA modification	1.19E-16	21	60	178	6381
0006364	rRNA processing	4.27E-14	24	60	341	6381
0016072	rRNA metabolic process	1.08E-13	24	60	356	6381
0000498	base pairing with RNA	2.47E-13	24	60	372	6381
0034470	ncRNA processing	2.47E-13	26	60	457	6381
0000496	base pairing	2.47E-13	24	60	373	6381
1990904	ribonucleoprotein complex	2.47E-13	31	60	707	6381
0030529	intracellular ribonucleoprotein complex	2.47E-13	31	60	707	6381
0000454	snoRNA guided rRNA pseudouridine synthesis	1.96E-11	6	60	6	6381
0034660	ncRNA metabolic process	2.97E-11	26	60	562	6381
0042254	ribosome biogenesis	3.22E-11	24	60	467	6381
0006396	RNA processing	7.79E-11	27	60	641	6381
0022613	ribonucleoprotein complex biogenesis	2.14E-10	25	60	562	6381
0031981	nuclear lumen	1.68E-08	28	60	872	6381
0032991	macromolecular complex	3.72E-07	42	60	2174	6381
0006725	cellular aromatic compound metabolic process	6.74E-07	39	60	1926	6381

0006139	nucleobase-containing compound metabolic process	7.43E-07	38	60	1842	6381
0046483	heterocycle metabolic process	8.29E-07	39	60	1943	6381
1901360	organic cyclic compound metabolic process	1.91E-06	39	60	1999	6381
0044428	nuclear part	4.18E-06	30	60	1273	6381
0043233	organelle lumen	5.25E-06	28	60	1135	6381
0070013	intracellular organelle lumen	5.25E-06	28	60	1135	6381
0031428	box C/D snoRNP complex	1.01E-05	7	60	52	6381
0016070	RNA metabolic process	1.34E-05	29	60	1266	6381
0031974	membrane-enclosed lumen	1.37E-05	28	60	1191	6381
0016074	snoRNA metabolic process	2.02E-05	7	60	58	6381
0003723	RNA binding	2.27E-05	26	60	1070	6381
0044085	cellular component biogenesis	2.68E-05	27	60	1156	6381
0043228	non-membrane-bounded organelle	8.54E-05	28	60	1307	6381
0043232	intracellular non-membrane-bounded organelle	8.54E-05	28	60	1307	6381
0043412	macromolecule modification	2.37E-04	21	60	839	6381
0090304	nucleic acid metabolic process	4.36E-04	30	60	1592	6381
0034641	cellular nitrogen compound metabolic process	5.17E-04	40	60	2564	6381
0098800	inner mitochondrial membrane protein complex	2.06E-03	6	60	83	6381
0003676	nucleic acid binding	2.06E-03	29	60	1634	6381
0098798	mitochondrial protein complex	2.38E-03	7	60	123	6381
0046034	ATP metabolic process	2.68E-03	6	60	88	6381
0006807	nitrogen compound metabolic process	2.68E-03	40	60	2736	6381
0009205	purine ribonucleoside triphosphate metabolic process	3.33E-03	6	60	92	6381
0009144	purine nucleoside triphosphate metabolic process	3.67E-03	6	60	94	6381
0009199	ribonucleoside triphosphate metabolic process	4.05E-03	6	60	96	6381
0015078	hydrogen ion transmembrane transporter activity	4.11E-03	5	60	62	6381
0010467	gene expression	6.11E-03	30	60	1837	6381
0009141	nucleoside triphosphate metabolic process	6.25E-03	6	60	105	6381
0009126	purine nucleoside monophosphate metabolic process	7.76E-03	6	60	110	6381
0009167	purine ribonucleoside monophosphate metabolic process	7.76E-03	6	60	110	6381
0009117	nucleotide metabolic process	1.24E-02	8	60	217	6381
0009060	aerobic respiration	1.36E-02	5	60	82	6381
0006753	nucleoside phosphate metabolic process	1.40E-02	8	60	222	6381
0009150	purine ribonucleotide metabolic process	1.43E-02	6	60	125	6381
0009161	ribonucleoside monophosphate metabolic process	1.45E-02	6	60	126	6381

0046128	purine ribonucleoside metabolic process	1.45E-02	6	60	126	6381
0042278	purine nucleoside metabolic process	1.48E-02	6	60	127	6381
0006163	purine nucleotide metabolic process	1.56E-02	6	60	129	6381
0009123	nucleoside monophosphate metabolic process	1.56E-02	6	60	129	6381
0015077	monovalent inorganic cation transmembrane transporter activity	1.66E-02	5	60	88	6381
0070069	cytochrome complex	1.70E-02	3	60	24	6381
0009259	ribonucleotide metabolic process	2.12E-02	6	60	138	6381
0009119	ribonucleoside metabolic process	2.25E-02	6	60	140	6381
0055086	nucleobase-containing small molecule metabolic process	2.36E-02	8	60	247	6381
0045333	cellular respiration	2.39E-02	5	60	97	6381
0044446	intracellular organelle part	2.40E-02	40	60	3034	6381
0044422	organelle part	2.66E-02	40	60	3049	6381
0072521	purine-containing compound metabolic process	3.09E-02	6	60	152	6381
0009116	nucleoside metabolic process	3.09E-02	6	60	152	6381
0098803	respiratory chain complex	3.09E-02	3	60	31	6381
0005746	mitochondrial respiratory chain	3.09E-02	3	60	31	6381
0042773	ATP synthesis coupled electron transport	3.09E-02	3	60	31	6381
0042775	mitochondrial ATP synthesis coupled electron transport	3.09E-02	3	60	31	6381
1901657	glycosyl compound metabolic process	3.49E-02	6	60	157	6381
0019693	ribose phosphate metabolic process	3.56E-02	6	60	158	6381
0022904	respiratory electron transport chain	3.57E-02	3	60	33	6381
0005634	nucleus	3.71E-02	33	60	2377	6381
0006119	oxidative phosphorylation	3.80E-02	3	60	34	6381
0000472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4.04E-02	3	60	35	6381
0070469	respiratory chain	4.04E-02	3	60	35	6381
0022900	electron transport chain	4.24E-02	3	60	36	6381
0000967	rRNA 5'-end processing	4.24E-02	3	60	36	6381
0034471	ncRNA 5'-end processing	4.24E-02	3	60	36	6381
0006091	generation of precursor metabolites and energy	4.36E-02	6	60	168	6381
0000966	RNA 5'-end processing	4.49E-02	3	60	37	6381
0045263	proton-transporting ATP synthase complex, coupling factor F(o)	4.80E-02	2	60	12	6381
0000276	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)	4.80E-02	2	60	12	6381
0030677	ribonuclease P complex	4.80E-02	2	60	12	6381

Table 3-A3. Full Gene Ontology terms based on down-regulated differentially expressed genes at 4 h in the S288C strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
0005732	small nucleolar ribonucleoprotein complex	4.30E-22	17	27	106	6381
0000944	base pairing with rRNA	5.07E-21	15	27	73	6381
0030555	RNA modification guide activity	2.04E-19	14	27	71	6381
0030556	rRNA modification guide activity	2.04E-19	14	27	71	6381
0030558	RNA pseudouridylation guide activity	1.00E-18	11	27	28	6381
0030559	rRNA pseudouridylation guide activity	1.00E-18	11	27	28	6381
0044452	nucleolar part	1.83E-18	16	27	148	6381
0031429	box H/ACA snoRNP complex	5.95E-18	11	27	33	6381
0072588	box H/ACA RNP complex	5.95E-18	11	27	33	6381
0031118	rRNA pseudouridine synthesis	7.90E-18	11	27	34	6381
0005697	telomerase holoenzyme complex	2.13E-17	11	27	37	6381
0019843	rRNA binding	2.82E-17	15	27	140	6381
0001522	pseudouridine synthesis	2.10E-16	11	27	45	6381
0000154	rRNA modification	2.71E-16	13	27	93	6381
0000454	snoRNA guided rRNA pseudouridine synthesis	8.35E-14	6	27	6	6381
1990904	ribonucleoprotein complex	5.91E-13	20	27	707	6381
0030529	intracellular ribonucleoprotein complex	5.91E-13	20	27	707	6381
0009451	RNA modification	1.26E-12	13	27	178	6381
0005730	nucleolus	1.52E-12	16	27	366	6381
0006364	rRNA processing	1.17E-11	15	27	341	6381
0016072	rRNA metabolic process	2.10E-11	15	27	356	6381
0000498	base pairing with RNA	3.80E-11	15	27	372	6381
0000496	base pairing	3.80E-11	15	27	373	6381
0022613	ribonucleoprotein complex biogenesis	5.54E-11	17	27	562	6381
0006396	RNA processing	4.51E-10	17	27	641	6381
0034470	ncRNA processing	6.37E-10	15	27	457	6381
0042254	ribosome biogenesis	8.37E-10	15	27	467	6381
0032991	macromolecular complex	4.21E-09	25	27	2174	6381
0034660	ncRNA metabolic process	1.09E-08	15	27	562	6381
0006139	nucleobase-containing compound metabolic process	2.27E-08	23	27	1842	6381
0006725	cellular aromatic compound metabolic process	5.74E-08	23	27	1926	6381

0046483	heterocycle metabolic process	6.71E-08	23	27	1943	6381
0003723	RNA binding	1.16E-07	18	27	1070	6381
1901360	organic cyclic compound metabolic process	1.16E-07	23	27	1999	6381
0044428	nuclear part	2.15E-07	19	27	1273	6381
0031981	nuclear lumen	4.26E-07	16	27	872	6381
0016074	snoRNA metabolic process	1.18E-06	6	27	58	6381
0034641	cellular nitrogen compound metabolic process	2.10E-06	24	27	2564	6381
0044085	cellular component biogenesis	2.99E-06	17	27	1156	6381
0006807	nitrogen compound metabolic process	8.40E-06	24	27	2736	6381
0016070	RNA metabolic process	1.11E-05	17	27	1266	6381
0043233	organelle lumen	1.52E-05	16	27	1135	6381
0070013	intracellular organelle lumen	1.52E-05	16	27	1135	6381
0031428	box C/D snoRNP complex	1.87E-05	5	27	52	6381
0031974	membrane-enclosed lumen	2.83E-05	16	27	1191	6381
0015078	hydrogen ion transmembrane transporter activity	4.33E-05	5	27	62	6381
0090304	nucleic acid metabolic process	4.70E-05	18	27	1592	6381
0044446	intracellular organelle part	6.67E-05	24	27	3034	6381
0003676	nucleic acid binding	6.71E-05	18	27	1634	6381
0044422	organelle part	7.13E-05	24	27	3049	6381
0043412	macromolecule modification	8.42E-05	13	27	839	6381
0043228	non-membrane-bounded organelle	8.53E-05	16	27	1307	6381
0043232	intracellular non-membrane-bounded organelle	8.53E-05	16	27	1307	6381
0098800	inner mitochondrial membrane protein complex	1.56E-04	5	27	83	6381
0015077	monovalent inorganic cation transmembrane transporter activity	2.00E-04	5	27	88	6381
0046034	ATP metabolic process	2.00E-04	5	27	88	6381
0009205	purine ribonucleoside triphosphate metabolic process	2.44E-04	5	27	92	6381
0009144	purine nucleoside triphosphate metabolic process	2.66E-04	5	27	94	6381
0009199	ribonucleoside triphosphate metabolic process	2.89E-04	5	27	96	6381
0010467	gene expression	3.17E-04	18	27	1837	6381
0009141	nucleoside triphosphate metabolic process	4.31E-04	5	27	105	6381
0009126	purine nucleoside monophosphate metabolic process	5.21E-04	5	27	110	6381
0009167	purine ribonucleoside monophosphate metabolic process	5.21E-04	5	27	110	6381
0070069	cytochrome complex	7.98E-04	3	27	24	6381
0098798	mitochondrial protein complex	8.59E-04	5	27	123	6381
0009150	purine ribonucleotide metabolic process	9.13E-04	5	27	125	6381

0046128	purine ribonucleoside metabolic process	9.20E-04	5	27	126	6381
0009161	ribonucleoside monophosphate metabolic process	9.20E-04	5	27	126	6381
0042278	purine nucleoside metabolic process	9.41E-04	5	27	127	6381
0006163	purine nucleotide metabolic process	9.84E-04	5	27	129	6381
0009123	nucleoside monophosphate metabolic process	9.84E-04	5	27	129	6381
0022890	inorganic cation transmembrane transporter activity	1.08E-03	5	27	132	6381
0009259	ribonucleotide metabolic process	1.31E-03	5	27	138	6381
0030627	pre-mRNA 5'-splice site binding	1.37E-03	2	27	6	6381
0009119	ribonucleoside metabolic process	1.37E-03	5	27	140	6381
0098803	respiratory chain complex	1.41E-03	3	27	31	6381
0005746	mitochondrial respiratory chain	1.41E-03	3	27	31	6381
0042773	ATP synthesis coupled electron transport	1.41E-03	3	27	31	6381
0042775	mitochondrial ATP synthesis coupled electron transport	1.41E-03	3	27	31	6381
0044238	primary metabolic process	1.61E-03	24	27	3614	6381
0022904	respiratory electron transport chain	1.66E-03	3	27	33	6381
0006119	oxidative phosphorylation	1.79E-03	3	27	34	6381
0072521	purine-containing compound metabolic process	1.79E-03	5	27	152	6381
0009116	nucleoside metabolic process	1.79E-03	5	27	152	6381
0070469	respiratory chain	1.88E-03	3	27	35	6381
0022900	electron transport chain	2.01E-03	3	27	36	6381
1901657	glycosyl compound metabolic process	2.01E-03	5	27	157	6381
0019693	ribose phosphate metabolic process	2.04E-03	5	27	158	6381
0005634	nucleus	2.13E-03	19	27	2377	6381
0044237	cellular metabolic process	2.30E-03	24	27	3699	6381
0000395	mRNA 5'-splice site recognition	2.65E-03	2	27	9	6381
0030561	RNA 2'-O-ribose methylation guide activity	3.17E-03	3	27	43	6381
0030562	rRNA 2'-O-ribose methylation guide activity	3.17E-03	3	27	43	6381
0044455	mitochondrial membrane part	3.21E-03	5	27	177	6381
0071840	cellular component organization or biogenesis	3.25E-03	19	27	2458	6381
0071704	organic substance metabolic process	3.46E-03	24	27	3787	6381
0009055	electron carrier activity	4.39E-03	3	27	49	6381
0036002	pre-mRNA binding	4.39E-03	2	27	12	6381
0045263	proton-transporting ATP synthase complex, coupling factor F(o)	4.39E-03	2	27	12	6381
0000276	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)	4.39E-03	2	27	12	6381

0006123	mitochondrial electron transport, cytochrome c to oxygen	5.12E-03	2	27	13	6381
0008324	cation transmembrane transporter activity	5.13E-03	5	27	200	6381
1901363	heterocyclic compound binding	5.13E-03	18	27	2324	6381
0097159	organic cyclic compound binding	5.41E-03	18	27	2335	6381
0045277	respiratory chain complex IV	5.63E-03	2	27	14	6381
0045292	mRNA cis splicing, via spliceosome	5.63E-03	2	27	14	6381
0005751	mitochondrial respiratory chain complex IV	5.63E-03	2	27	14	6381
0009117	nucleotide metabolic process	6.97E-03	5	27	217	6381
0006376	mRNA splice site selection	7.25E-03	2	27	16	6381
0006753	nucleoside phosphate metabolic process	7.57E-03	5	27	222	6381
0008152	metabolic process	7.90E-03	24	27	3978	6381
0045259	proton-transporting ATP synthase complex	7.90E-03	2	27	17	6381
0005753	mitochondrial proton-transporting ATP synthase complex	7.90E-03	2	27	17	6381
0033177	proton-transporting two-sector ATPase complex, proton-transporting domain	9.63E-03	2	27	19	6381
0015985	energy coupled proton transport, down electrochemical gradient	9.63E-03	2	27	19	6381
0015986	ATP synthesis coupled proton transport	9.63E-03	2	27	19	6381
0004129	cytochrome-c oxidase activity	1.03E-02	2	27	20	6381
0016675	oxidoreductase activity, acting on a heme group of donors	1.03E-02	2	27	20	6381
0016676	oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor	1.03E-02	2	27	20	6381
0015002	heme-copper terminal oxidase activity	1.03E-02	2	27	20	6381
0055086	nucleobase-containing small molecule metabolic process	1.10E-02	5	27	247	6381
0006754	ATP biosynthetic process	1.12E-02	2	27	21	6381
0005743	mitochondrial inner membrane	1.14E-02	5	27	250	6381
0019646	aerobic electron transport chain	1.35E-02	1	27	1	6381
0019866	organelle inner membrane	1.37E-02	5	27	262	6381
0009145	purine nucleoside triphosphate biosynthetic process	1.40E-02	2	27	24	6381
0009206	purine ribonucleoside triphosphate biosynthetic process	1.40E-02	2	27	24	6381
0009060	aerobic respiration	1.48E-02	3	27	82	6381
0005488	binding	1.54E-02	21	27	3306	6381
0015075	ion transmembrane transporter activity	1.54E-02	5	27	272	6381
0044260	cellular macromolecule metabolic process	1.73E-02	19	27	2835	6381
0009201	ribonucleoside triphosphate biosynthetic process	1.83E-02	2	27	28	6381
0045333	cellular respiration	2.28E-02	3	27	97	6381

0016469	proton-transporting two-sector ATPase complex	2.32E-02	2	27	32	6381
0009142	nucleoside triphosphate biosynthetic process	2.32E-02	2	27	32	6381
0045153	electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex activity	2.46E-02	1	27	2	6381
0000245	spliceosomal complex assembly	2.57E-02	2	27	34	6381
0098796	membrane protein complex	2.61E-02	5	27	313	6381
0043170	macromolecule metabolic process	2.62E-02	19	27	2938	6381
1902600	hydrogen ion transmembrane transport	2.64E-02	2	27	35	6381
0000472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2.64E-02	2	27	35	6381
0034471	ncRNA 5'-end processing	2.75E-02	2	27	36	6381
0000967	rRNA 5'-end processing	2.75E-02	2	27	36	6381
0022891	substrate-specific transmembrane transporter activity	2.81E-02	5	27	322	6381
0000966	RNA 5'-end processing	2.86E-02	2	27	37	6381
0009127	purine nucleoside monophosphate biosynthetic process	3.94E-02	2	27	44	6381
0009168	purine ribonucleoside monophosphate biosynthetic process	3.94E-02	2	27	44	6381
0015992	proton transport	4.08E-02	2	27	45	6381
0000447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4.20E-02	2	27	46	6381
0006818	hydrogen transport	4.20E-02	2	27	46	6381
0022857	transmembrane transporter activity	4.21E-02	5	27	360	6381
1901135	carbohydrate derivative metabolic process	4.30E-02	5	27	363	6381
0016679	oxidoreductase activity, acting on diphenols and related substances as donors	4.30E-02	1	27	4	6381
0016681	oxidoreductase activity, acting on diphenols and related substances as donors, cytochrome as acceptor	4.30E-02	1	27	4	6381
0008121	ubiquinol-cytochrome-c reductase activity	4.30E-02	1	27	4	6381
0043231	intracellular membrane-bounded organelle	4.35E-02	24	27	4429	6381
0043227	membrane-bounded organelle	4.51E-02	24	27	4439	6381
0046129	purine ribonucleoside biosynthetic process	4.82E-02	2	27	51	6381
0042451	purine nucleoside biosynthetic process	4.82E-02	2	27	51	6381

Table 3-A4. Full Gene Ontology terms based on up-regulated differentially expressed genes at 1 h in the S7 strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
0030555	RNA modification guide activity	2.28E-04	3	4	71	6381
0030556	rRNA modification guide activity	2.28E-04	3	4	71	6381
0000944	base pairing with rRNA	2.28E-04	3	4	73	6381
0005732	small nucleolar ribonucleoprotein complex	5.28E-04	3	4	106	6381
0019843	rRNA binding	9.62E-04	3	4	140	6381
0044452	nucleolar part	9.62E-04	3	4	148	6381
0030558	RNA pseudouridylation guide activity	1.52E-03	2	4	28	6381
0030559	rRNA pseudouridylation guide activity	1.52E-03	2	4	28	6381
0030529	intracellular ribonucleoprotein complex	1.52E-03	4	4	707	6381
1990904	ribonucleoprotein complex	1.52E-03	4	4	707	6381
0072588	box H/ACA RNP complex	1.52E-03	2	4	33	6381
0031429	box H/ACA snoRNP complex	1.52E-03	2	4	33	6381
0031118	rRNA pseudouridine synthesis	1.52E-03	2	4	34	6381
0005697	telomerase holoenzyme complex	1.67E-03	2	4	37	6381
0001522	pseudouridine synthesis	2.31E-03	2	4	45	6381
0005730	nucleolus	5.06E-03	3	4	366	6381
0000498	base pairing with RNA	5.06E-03	3	4	372	6381
0000496	base pairing	5.06E-03	3	4	373	6381
0000154	rRNA modification	7.81E-03	2	4	93	6381
0000454	snoRNA guided rRNA pseudouridine synthesis	2.25E-02	1	4	6	6381
0048500	signal recognition particle	2.33E-02	1	4	7	6381
0005786	signal recognition particle, endoplasmic reticulum targeting	2.33E-02	1	4	7	6381
0009451	RNA modification	2.33E-02	2	4	178	6381
0031981	nuclear lumen	4.57E-02	3	4	872	6381
0006616	SRP-dependent cotranslational protein targeting to membrane, translocation	4.80E-02	1	4	16	6381

Table 3-A5. Full Gene Ontology terms based on down-regulated differentially expressed genes at 1 h in the S7 strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
0009277	fungal-type cell wall	2.98E-07	8	22	108	6381
0005618	cell wall	2.98E-07	8	22	114	6381
0030312	external encapsulating structure	2.98E-07	8	22	114	6381
0005576	extracellular region	3.15E-07	8	22	119	6381
0031225	anchored component of membrane	6.33E-03	4	22	68	6381

Table 3-A6. Full Gene Ontology terms based on up-regulated differentially expressed genes at 4 h in the S7 strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
0000943	retrotransposon nucleocapsid	7.39E-03	2	2	92	6381
0032197	transposition, RNA-mediated	7.39E-03	2	2	93	6381
0032196	transposition	7.39E-03	2	2	99	6381

Table 3-A7. Full Gene Ontology terms based on down-regulated differentially expressed genes at 4 h in the S7 strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
0030555	RNA modification guide activity	1.62E-04	3	4	71	6381
0030556	rRNA modification guide activity	1.62E-04	3	4	71	6381
0000944	base pairing with rRNA	1.62E-04	3	4	73	6381
0000154	rRNA modification	2.52E-04	3	4	93	6381
0005732	small nucleolar ribonucleoprotein complex	2.99E-04	3	4	106	6381
0019843	rRNA binding	5.77E-04	3	4	140	6381
0044452	nucleolar part	5.84E-04	3	4	148	6381
0009451	RNA modification	8.89E-04	3	4	178	6381
0030558	RNA pseudouridylation guide activity	9.42E-04	2	4	28	6381
0030559	rRNA pseudouridylation guide activity	9.42E-04	2	4	28	6381
0072588	box H/ACA RNP complex	1.07E-03	2	4	33	6381
0031429	box H/ACA snoRNP complex	1.07E-03	2	4	33	6381
0031118	rRNA pseudouridine synthesis	1.07E-03	2	4	34	6381
0005697	telomerase holoenzyme complex	1.18E-03	2	4	37	6381
0001522	pseudouridine synthesis	1.64E-03	2	4	45	6381
0006364	rRNA processing	3.09E-03	3	4	341	6381
0016072	rRNA metabolic process	3.22E-03	3	4	356	6381
0005730	nucleolus	3.22E-03	3	4	366	6381
0000498	base pairing with RNA	3.22E-03	3	4	372	6381
0000496	base pairing	3.22E-03	3	4	373	6381
0034470	ncRNA processing	5.60E-03	3	4	457	6381
0042254	ribosome biogenesis	5.69E-03	3	4	467	6381
0022613	ribonucleoprotein complex biogenesis	9.00E-03	3	4	562	6381
0034660	ncRNA metabolic process	9.00E-03	3	4	562	6381
0006396	RNA processing	1.23E-02	3	4	641	6381
0000454	snoRNA guided rRNA pseudouridine synthesis	1.23E-02	1	4	6	6381
0030529	intracellular ribonucleoprotein complex	1.51E-02	3	4	707	6381
1990904	ribonucleoprotein complex	1.51E-02	3	4	707	6381
0043412	macromolecule modification	2.40E-02	3	4	839	6381
0031981	nuclear lumen	2.59E-02	3	4	872	6381
0003723	RNA binding	4.51E-02	3	4	1070	6381

Table 3-A8. Full Gene Ontology terms based on up-regulated differentially expressed genes at 1 h in the MS300c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
0035873	lactate transmembrane transport	2.57E-02	1	4	1	6381
0035879	plasma membrane lactate transport	2.57E-02	1	4	1	6381
0006849	plasma membrane pyruvate transport	2.57E-02	1	4	1	6381
0015727	lactate transport	2.57E-02	1	4	1	6381
0015355	secondary active monocarboxylate transmembrane transporter activity	2.57E-02	1	4	1	6381
0000943	retrotransposon nucleocapsid	3.19E-02	2	4	92	6381
0032197	transposition, RNA-mediated	3.19E-02	2	4	93	6381
0097079	selenite:proton symporter activity	3.19E-02	1	4	2	6381
0032196	transposition	3.19E-02	2	4	99	6381
0097080	plasma membrane selenite transport	3.85E-02	1	4	3	6381
1901475	pyruvate transmembrane transport	4.67E-02	1	4	4	6381

Table 3-A9. Full Gene Ontology terms based on down-regulated differentially expressed genes at 1 h in the MS300c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
0019058	viral life cycle	1.93E-02	2	6	45	6381
0019076	viral release from host cell	1.93E-02	2	6	45	6381
0016032	viral process	1.93E-02	2	6	45	6381
0044403	symbiosis, encompassing mutualism through parasitism	1.93E-02	2	6	45	6381
0004523	RNA-DNA hybrid ribonuclease activity	1.93E-02	2	6	48	6381
0015074	DNA integration	1.93E-02	2	6	50	6381
0044419	interspecies interaction between organisms	1.93E-02	2	6	51	6381
0006146	adenine catabolic process	1.93E-02	1	6	1	6381
0046101	hypoxanthine biosynthetic process	1.93E-02	1	6	1	6381
0000034	adenine deaminase activity	1.93E-02	1	6	1	6381
0043103	hypoxanthine salvage	1.93E-02	1	6	1	6381
0003964	RNA-directed DNA polymerase activity	1.93E-02	2	6	52	6381
0004190	aspartic-type endopeptidase activity	1.93E-02	2	6	55	6381
0070001	aspartic-type peptidase activity	1.93E-02	2	6	55	6381
0003887	DNA-directed DNA polymerase activity	2.22E-02	2	6	63	6381
0016891	endoribonuclease activity, producing 5'-phosphomonoesters	2.22E-02	2	6	63	6381
0034061	DNA polymerase activity	2.36E-02	2	6	67	6381
0016893	endonuclease activity	2.38E-02	2	6	71	6381
0006145	purine nucleobase catabolic process	2.38E-02	1	6	2	6381
0046100	hypoxanthine metabolic process	2.38E-02	1	6	2	6381
0004521	endoribonuclease activity	2.45E-02	2	6	76	6381
0043096	purine nucleobase salvage	3.07E-02	1	6	3	6381
0000943	retrotransposon nucleocapsid	3.07E-02	2	6	92	6381
0004540	ribonuclease activity	3.07E-02	2	6	93	6381
0032197	transposition, RNA-mediated	3.07E-02	2	6	93	6381
0032196	transposition	3.34E-02	2	6	99	6381
0046113	nucleobase catabolic process	3.52E-02	1	6	4	6381
0046083	adenine metabolic process	4.24E-02	1	6	5	6381
0004519	endonuclease activity	4.37E-02	2	6	120	6381
0004175	endopeptidase activity	4.50E-02	2	6	124	6381
0016779	nucleotidyltransferase activity	4.85E-02	2	6	131	6381

Table 3-A10. Full Gene Ontology terms based on down-regulated differentially expressed genes at 4 h in the MS300c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
0030555	RNA modification guide activity	2.50E-06	5	10	71	6381
0030556	rRNA modification guide activity	2.50E-06	5	10	71	6381
0000944	base pairing with rRNA	2.50E-06	5	10	73	6381
0030558	RNA pseudouridylation guide activity	2.50E-06	4	10	28	6381
0030559	rRNA pseudouridylation guide activity	2.50E-06	4	10	28	6381
0031429	box H/ACA snoRNP complex	3.52E-06	4	10	33	6381
0072588	box H/ACA RNP complex	3.52E-06	4	10	33	6381
0031118	rRNA pseudouridine synthesis	3.52E-06	4	10	34	6381
0005697	telomerase holoenzyme complex	4.44E-06	4	10	37	6381
0005732	small nucleolar ribonucleoprotein complex	5.54E-06	5	10	106	6381
0001522	pseudouridine synthesis	8.15E-06	4	10	45	6381
0019843	rRNA binding	1.86E-05	5	10	140	6381
0044452	nucleolar part	2.26E-05	5	10	148	6381
0000154	rRNA modification	1.21E-04	4	10	93	6381
1990904	ribonucleoprotein complex	2.26E-04	7	10	707	6381
0030529	intracellular ribonucleoprotein complex	2.26E-04	7	10	707	6381
0000454	snoRNA guided rRNA pseudouridine synthesis	3.97E-04	2	10	6	6381
0009451	RNA modification	1.22E-03	4	10	178	6381
0005730	nucleolus	1.27E-03	5	10	366	6381
0000498	base pairing with RNA	1.27E-03	5	10	372	6381
0000496	base pairing	1.27E-03	5	10	373	6381
0003723	RNA binding	2.55E-03	7	10	1070	6381
0044428	nuclear part	7.47E-03	7	10	1273	6381
0022613	ribonucleoprotein complex biogenesis	7.67E-03	5	10	562	6381
0006364	rRNA processing	1.06E-02	4	10	341	6381
0016072	rRNA metabolic process	1.20E-02	4	10	356	6381
0006396	RNA processing	1.25E-02	5	10	641	6381
0016074	snoRNA metabolic process	2.54E-02	2	10	58	6381
0034470	ncRNA processing	2.71E-02	4	10	457	6381
0003676	nucleic acid binding	2.74E-02	7	10	1634	6381
0042254	ribosome biogenesis	2.74E-02	4	10	467	6381
0031981	nuclear lumen	4.17E-02	5	10	872	6381

Table 3-A11. Numbers of variant callings in the transcripts of *snR34*, *snR35*, and *snR37* genes in the S288C strain exposed to ribavirin for 1 h and their respective negative controls.

Gene	Sample	Replicate	Number of detected nucleotide (nt)	Number of variant callings (nt)	Percentage of variant callings (%)
snR34	Ctrl 1hr	1	53567	59	0.11
		2	12489	47	0.38
		3	12449	29	0.23
		Mean (SD)	26168 (23728)	45 (15)	0.24 (0.13)
	Riba 1hr	1	84380	74	0.09
		2	7498	9	0.12
		3	31990	82	0.26
		Mean (SD)	41289 (39276)	55 (40)	0.15 (0.09)
snR35	Ctrl 1hr	1	49762	64	0.13
		2	12215	22	0.18
		3	12775	33	0.26
		Mean (SD)	24917 (21518)	40 (22)	0.19 (0.07)
	Riba 1hr	1	84834	133	0.16
		2	7304	14	0.19
		3	22295	66	0.30
		Mean (SD)	38144 (41123)	71 (60)	0.21 (0.07)
snR37	Ctrl 1hr	1	195149	311	0.16
		2	34685	56	0.16
		3	37993	76	0.20
		Mean (SD)	89276 (91704)	148 (142)	0.17 (0.02)
	Riba 1hr	1	288752	226	0.08
		2	32240	56	0.17
		3	137139	255	0.19
		Mean (SD)	152710 (128963)	179 (108)	0.15 (0.06)

Table 4-A1. FPKM values of the differentially expressed genes in the S288C strain.

Gene	Gene short name	1 h			4 h		
		Blank	Exposed	P value	Blank	Exposed	P value
S000003269	ACB1	471.682	1358.78	5.00E-05	520.635	1295.92	5.00E-05
S000005299	ACC1	49.3194	101.429	0.0002			
S000004295	ACO1	2077.36	403.211	5.00E-05	1756.38	310.356	5.00E-05
S000000050	ACS1	244.938	80.0626	5.00E-05	627.551	51.127	5.00E-05
S000004915	ADE4	22.0976	9.70298	5.00E-05	25.6602	6.45342	5.00E-05
S000028518	ADF1	32.1279	14.4872	0.0227	41.6711	17.4351	0.00475
S000004611	ADI1	134.63	296.128	5.00E-05			
S000004099	AHP1	1246.83	2822.45	0.00075	460.419	2470.7	5.00E-05
S000001013	AIM17	410.545	1140.92	5.00E-05	167.432	937.176	5.00E-05
S000003658	ALB1	65.9847	14.0819	5.00E-05	45.1201	7.70659	5.00E-05
S000004779	ALD3	36.1345	388.806	5.00E-05	24.0343	272.439	5.00E-05
S000005901	ALD4	636.374	1295.43	0.0016			
S000000875	ALD5	12.5875	34.0831	5.00E-05			
S000005982	ALD6	1202.22	2699.86	5.00E-05			
S000003808	ANB1	3.20749	15.9214	5.00E-05			
S000000555	APA1	65.0547	131.24	5.00E-05	41.9152	115.888	5.00E-05
S000005116	APC1	9.35501	4.27576	5.00E-05			
S000000355	APD1	223.09	847.394	5.00E-05	149.544	717.241	5.00E-05
S000005021	APJ1	83.153	457.38	5.00E-05	64.5934	435.714	5.00E-05
S000006396	AQY1	178.758	83.5021	5.00E-05			
S000005302	ARE2	64.6583	138.99	5.00E-05	49.2348	119.387	5.00E-05
S000002788	ARO10	295.657	52.256	5.00E-05	287.824	35.684	5.00E-05
S000002513	ARP10	3.14285	1.56852	0.0076	4.46499	1.41234	0.00015
S000002508	ARX1	33.4618	14.1036	5.00E-05	22.7119	7.82249	5.00E-05
S000006171	ATG41	43.7969	298.49	5.00E-05	37.4574	289.085	5.00E-05
S000000790	AVT2	25.4494	9.8033	5.00E-05	36.3407	8.624	5.00E-05
S000000056	BDH1	611.664	1836.12	5.00E-05	341.752	1584.45	5.00E-05
S000000057	BDH2	402.654	916.382	5.00E-05	224.38	738.351	5.00E-05
S000002707	BFR2	37.1098	15.2498	5.00E-05	30.4921	10.6643	5.00E-05
S000003518	BIO2	20.9292	45.9594	5.00E-05			
S000004053	BMT6	15.058	6.2148	5.00E-05	11.4563	5.49955	5.00E-05
S000001943	BNA6	251.419	512.247	5.00E-05			
S000000181	BOI1	7.03934	14.623	5.00E-05			
S000005437	BRX1	80.3957	32.1452	5.00E-05	55.7297	25.3675	5.00E-05
S000002683	BSC2	191.861	94.8235	5.00E-05	247.932	58.7454	5.00E-05
S000003374	BTN2	34.4472	1110.39	5.00E-05	36.9271	1582.5	5.00E-05
S000006032	CAR1	58.4739	125.54	5.00E-05	35.6043	90.1428	5.00E-05
S000003268	CAX4	18.7229	59.6953	5.00E-05	27.0892	70.2184	5.00E-05
S000003372	CBF2	6.72303	3.35138	5.00E-05	9.58376	2.97539	5.00E-05
S000002227	CBS1	27.0457	11.0094	5.00E-05	25.6565	8.71483	5.00E-05
S000003449	CCH1	5.89959	2.71902	5.00E-05	5.89318	2.58644	5.00E-05
S000003647	CCT7	73.7952	35.1606	5.00E-05			
S000004306	CDC3	33.3472	72.1339	5.00E-05			
S000005783	CDC31	175.02	351.317	5.00E-05			
S000006081	CDC60	24.3432	11.1359	5.00E-05	20.6087	9.58768	5.00E-05
S000002971	CDH1	70.0302	33.743	5.00E-05			
S000000242	CHS2	13.7926	29.5161	5.00E-05	12.2676	26.3132	5.00E-05
S000001094	CIC1	51.6954	17.367	5.00E-05	28.342	10.7152	5.00E-05
S000004338	CIS1	61.2626	3264.9	5.00E-05	40.9623	2780.03	5.00E-05
S000004123	CKI1	48.7784	106.419	5.00E-05	44.9295	102.334	5.00E-05
S000004812	CLN1	30.589	8.33358	5.00E-05	73.0736	7.17175	5.00E-05
S000000038	CLN3	42.8245	15.256	5.00E-05	52.006	13.1664	5.00E-05
S000005376	CMK2	115.08	381.838	5.00E-05			
S000002315	CMR1	8.46007	4.01773	5.00E-05	11.5736	3.9961	5.00E-05
S000000932	COM2	24.9821	58.9052	5.00E-05			
S000005324	COQ2	25.3953	11.8584	5.00E-05			
S000005280	COS1	45.6705	97.6192	5.00E-05			
S000005358	COS10	3.03452	8.32953	5.00E-05			
S000006093	COX10	16.7879	7.15891	5.00E-05			
S000001373	COX5B	204.674	616.87	5.00E-05	85.5281	503.594	5.00E-05
S000003479	CPD1	42.1084	98.9426	5.00E-05	27.1808	94.0943	5.00E-05
S000004206	CPR6	637.552	1338.8	0.00055	251.301	1118.93	5.00E-05

S000001189	CRP1	150.493	336.451	5.00E-05			
S000004203	CRR1	14.5424	7.00332	5.00E-05	30.7957	8.0411	5.00E-05
S000002558	CTH1	77.816	230.949	5.00E-05	63.9378	226.075	5.00E-05
S000006328	CTR1	991.266	417.679	5.00E-05			
S000004276	CTS1	488.61	1156.9	5.00E-05	170.017	1208.45	5.00E-05
S000002779	CTS2	7.07201	15.9209	5.00E-05	4.78614	16.2217	5.00E-05
S000003320	CTT1	254.18	591.212	0.0001			
S000006362	CUR1	12.7761	60.6488	5.00E-05	11.9188	63.2889	5.00E-05
S000002368	CWC2	16.3023	7.27641	5.00E-05	16.665	5.7145	5.00E-05
S000001579	CWP1	193.907	89.4055	5.00E-05	330.559	83.5951	5.00E-05
S000005055	CYB5	25.4567	8.81733	5.00E-05	31.34	10.6744	5.00E-05
S000000765	CYC7	414.382	2352.94	5.00E-05	96.2173	2061.69	5.00E-05
S000004535	DAK1	110.071	222.891	5.00E-05			
S000001841	DAK2	3.58033	7.19463	5.00E-05	2.13084	9.40747	5.00E-05
S000006091	DAP1	144.592	615.145	5.00E-05	150.582	715.836	5.00E-05
S000005056	DBP2	63.0855	23.6424	5.00E-05	51.0876	16.899	5.00E-05
S000003046	DBP3	67.2477	29.2498	5.00E-05	44.6698	19.911	5.00E-05
S000005321	DBP6	24.1569	11.6008	5.00E-05			
S000001732	DBP7	12.1696	4.9507	5.00E-05	9.49572	3.16592	5.00E-05
S000001212	DBP8	14.744	7.0734	5.00E-05	11.8637	5.67492	5.00E-05
S000001187	DCD1	8.694	2.65497	5.00E-05	7.64133	1.86591	5.00E-05
S000005699	DCS2	466.292	1003.19	0.00055	336.88	931.512	5.00E-05
S000004784	DDR48	307.842	1026.11	5.00E-05	346.295	974.531	5.00E-05
S000005730	DED1	59.2447	217.04	5.00E-05	66.1286	135.113	5.00E-05
S000001561	DHR2	4.62505	1.36896	5.00E-05	3.02125	0.84211	5.00E-05
S000004935	DIA1	25.0931	90.2377	5.00E-05			
S000004429	DIF1	13.1756	83.7227	5.00E-05	14.5826	66.0216	5.00E-05
S000004119	DIP2	20.8657	6.4153	5.00E-05	16.1305	4.94349	5.00E-05
S000006186	DIP5	325.319	142.651	5.00E-05	305.53	92.569	5.00E-05
S000001085	DOG2	55.2679	248.005	5.00E-05	61.4334	245.485	5.00E-05
S000000890	DOT6	194.577	504.72	5.00E-05	139.699	408.093	5.00E-05
S000003931	DRS1	34.5858	17.2785	5.00E-05			
S000000796	DSF1	10.558	35.0727	5.00E-05	3.68941	48.0956	5.00E-05
S000004545	DUS1	16.0942	6.0406	5.00E-05	12.7027	3.93606	5.00E-05
S000000055	ECM1	45.9221	19.8641	5.00E-05			
S000004735	ECM16	18.9905	8.70993	5.00E-05	17.1543	7.94048	5.00E-05
S000005618	ECM3	34.2414	14.8811	5.00E-05			
S000007608	EFG1	30.7657	13.9542	5.00E-05	34.7309	14.1503	5.00E-05
S000007525	EGO4	4004.44	15738.5	5.00E-05	6197.81	14210.8	0.0001
S000004176	EMG1	32.1991	14.8518	5.00E-05	31.3053	11.9679	5.00E-05
S000002924	EMI2	120.936	589.202	5.00E-05	96.5434	582.993	5.00E-05
S000004073	EMP70	27.6672	11.6087	5.00E-05	28.3075	9.57352	5.00E-05
S000005257	EMW1	15.7612	4.51154	5.00E-05	15.3244	3.62734	5.00E-05
S000004652	ERB1	26.5123	11.237	5.00E-05	18.3413	8.4278	5.00E-05
S000004236	ERF2	67.7348	32.6848	5.00E-05	66.2612	25.7341	5.00E-05
S000003407	ERG1	173.563	79.596	5.00E-05	208.2	62.377	5.00E-05
S000001049	ERG11	190.025	75.0441	5.00E-05	185.139	65.6269	5.00E-05
S000004595	ERG13	86.7225	32.2004	5.00E-05	101.8	26.8205	5.00E-05
S000003292	ERG25	163.927	69.7075	5.00E-05	186.789	53.7845	5.00E-05
S000004046	ERG3	230.944	54.0273	5.00E-05	229.029	49.9643	5.00E-05
S000004617	ERG5	99.4785	19.1011	5.00E-05	77.7661	16.3099	5.00E-05
S000004599	ERO1	20.3913	61.365	5.00E-05	14.0755	37.4264	5.00E-05
S000005844	FAA1	242.435	502.288	0.0002	180.61	418.375	5.00E-05
S000004860	FAA4	35.5259	80.088	5.00E-05			
S000003693	FAR1	21.1354	8.2938	5.00E-05	17.6811	7.11882	5.00E-05
S000006152	FAS2	101.682	215.906	0.0001			
S000000858	FCY2	271.492	116.852	5.00E-05	232.921	57.8978	5.00E-05
S000006196	FDH2	8.35288	1.83635	5.00E-05	18.8902	1.55282	5.00E-05
S000000305	FES1	203.877	932.335	5.00E-05	192.087	935.564	5.00E-05
S000006200	FEX2	1.34508	0.626423	0.02185	1.82733	0.60128	0.0017
S000005909	FIT2	480.515	1080.71	5.00E-05	272.128	841.001	5.00E-05
S000004446	FMP27	25.9699	54.2077	5.00E-05	21.2382	54.0952	5.00E-05
S000005330	FPK1	17.8441	36.3847	5.00E-05			
S000004204	FRE1	32.3664	14.9449	5.00E-05			
S000005512	FRE7	96.0373	16.8064	5.00E-05			
S000004050	FRS1	52.1915	16.5936	5.00E-05	43.7337	13.3042	5.00E-05

S000000225	FUR4	38.4217	11.1237	5.00E-05	28.781	10.7469	5.00E-05
S000001747	GAP1	53.7311	13.4663	5.00E-05	98.1673	7.8744	5.00E-05
S000005646	GCY1	357.582	845.705	5.00E-05	201.973	727.392	5.00E-05
S000006388	GDB1	72.3244	165.241	0.0001	44.3307	174.425	5.00E-05
S000000541	GFD2	45.1735	6.64839	5.00E-05	13.4797	6.41447	5.00E-05
S000002915	GIN4	8.7989	4.28158	5.00E-05	17.8788	3.50614	5.00E-05
S000000856	GIP2	42.5941	100.214	5.00E-05	20.0933	102.045	5.00E-05
S000006058	GIP3	20.1735	102.265	5.00E-05	17.3004	79.4457	5.00E-05
S000002503	GIS1	57.0301	123.708	5.00E-05	39.4855	94.885	5.00E-05
S000000695	GIT1	18.0005	7.16824	5.00E-05	26.6394	5.28661	5.00E-05
S000000737	GLC3	481.241	214.239	5.00E-05	409.023	203.018	5.00E-05
S000000545	GLK1	2976.51	6020.78	0.0078	1620.71	5102.16	5.00E-05
S000001226	GND1	60.2047	209.68	5.00E-05	51.9877	158.673	5.00E-05
S000005218	GOR1	124.06	313.015	5.00E-05			
S000006364	GPH1	123.583	748.216	5.00E-05	135.421	859.65	5.00E-05
S000004894	GPI12	34.8484	72.1776	5.00E-05	21.6622	59.5787	5.00E-05
S000003958	GRC3	4.81788	2.15797	5.00E-05	4.60859	2.11586	5.00E-05
S000006144	GRE1	3031.47	588.561	5.00E-05	3337.04	427.285	5.00E-05
S000001146	GRE3	238.572	712.371	5.00E-05	142.247	638.294	5.00E-05
S000003637	GSH1	43.2867	89.8699	5.00E-05	30.0437	87.7304	5.00E-05
S000001911	GSY1	77.7108	169.427	0.0001	53.024	193.827	5.00E-05
S000004248	GSY2	263.493	758.131	5.00E-05	232.428	759.503	5.00E-05
S000002393	GYP7	98.9079	208.077	5.00E-05			
S000001863	HAC1	135.269	1069.42	5.00E-05	113.364	820.763	5.00E-05
S000004903	HAS1	29.0446	12.4105	5.00E-05	18.2642	8.37277	5.00E-05
S000005922	HAT1	8.06103	3.23391	5.00E-05	8.84229	3.04869	5.00E-05
S000007548	HBN1	12.1251	26.4106	5.00E-05			
S000000661	HCM1	7.23752	3.24182	5.00E-05	9.39762	2.73945	5.00E-05
S000005702	HEM15	93.8302	206.407	5.00E-05			
S000003419	HGH1	24.9275	11.5073	5.00E-05	26.2698	11.4329	5.00E-05
S000000452	HIS7	22.7851	5.54174	5.00E-05	25.6787	4.06025	5.00E-05
S000002828	HKR1	34.5938	11.8796	5.00E-05	21.0245	9.88873	5.00E-05
S000000238	HMT1	74.599	27.1854	5.00E-05	36.9771	14.1892	5.00E-05
S000004635	HOF1	7.3173	15.542	5.00E-05			
S000004103	HOG1	79.9027	175.612	5.00E-05	58.947	143.731	5.00E-05
S000004864	HOR7	6879.51	17325.1	5.00E-05			
S000002807	HPT1	174.111	69.644	5.00E-05	122.546	57.9612	5.00E-05
S000003949	HSP104	561.928	1863.09	5.00E-05	370.594	2051.44	5.00E-05
S000000615	HSP30	5626.25	19973.1	5.00E-05	1866.62	7232.96	5.00E-05
S000006201	HSP32	2.50448	1.00965	0.00745	4.16425	0.785736	0.0001
S000005918	HSP33	7.70647	2.68036	5.00E-05	15.117	2.69251	5.00E-05
S000002578	HSP42	830.307	2981.84	5.00E-05	539.502	3213.65	5.00E-05
S000002666	HSP78	237.692	487.745	0.00155	130.562	608.399	5.00E-05
S000006161	HSP82	612.426	1571.09	0.0008	235.182	1508.93	5.00E-05
S000002599	HST4	8.89403	3.65282	5.00E-05	9.30124	2.9503	5.00E-05
S000001949	HXK1	406.311	4288.88	5.00E-05	334.689	5182.73	5.00E-05
S000004613	HXT2	16.293	44.0906	5.00E-05			
S000001134	HXT4	8.0264	21.8245	5.00E-05	7.15708	14.6013	5.00E-05
S000001138	HXT5	1444.41	358.33	5.00E-05	963.804	203.234	5.00E-05
S000002751	HXT6	191.253	476.061	5.00E-05	83.8019	270.71	5.00E-05
S000002750	HXT7	33.1334	81.7562	5.00E-05	11.2244	36.6677	5.00E-05
S000004347	ILV5	203.67	39.6974	5.00E-05	138.03	18.9725	5.00E-05
S000003752	IMA5	1.64122	5.51734	5.00E-05			
S000001259	IMD2	14.89	64.2407	5.00E-05	24.7034	64.9761	5.00E-05
S000003618	IML2	39.9306	104.426	5.00E-05	25.3909	106.881	5.00E-05
S000001191	IMP3	40.9601	20.3234	5.00E-05	28.0077	11.4478	5.00E-05
S000004405	INA1	2.83775	8.80946	5.00E-05			
S000004817	INP1	27.5372	7.23326	5.00E-05	29.4852	6.95187	5.00E-05
S000001127	IPI1	12.1075	5.83679	5.00E-05	9.84844	3.86285	5.00E-05
S000005126	IPI3	16.9436	8.43888	5.00E-05	11.9272	5.78425	5.00E-05
S000005441	IRA2	59.9673	140.342	5.00E-05	35.1612	147.083	5.00E-05
S000005375	IRC10	4.73271	10.3265	5.00E-05	3.62025	10.5824	5.00E-05
S000005570	IRC23	78.9801	32.981	5.00E-05	72.1304	24.2245	5.00E-05
S000178119	IRT1	37.9469	94.6296	5.00E-05	34.7222	77.0709	5.00E-05
S000004686	ISF1	348.041	849.83	5.00E-05	179.398	798.976	5.00E-05
S000006056	ISU1	675.107	5453.18	5.00E-05	546.162	4355.32	5.00E-05

S000005362	IZH2	39.4091	101.429	5.00E-05	53.7118	108.515	5.00E-05
S000005461	IZH4	17.4828	127.119	5.00E-05	42.3896	119.34	5.00E-05
S000000912	KAP123	34.411	13.6578	5.00E-05	28.7295	10.0306	5.00E-05
S000004339	KAP95	37.8612	94.7546	5.00E-05	29.7977	83.6161	5.00E-05
S000003571	KAR2	109.442	432.833	5.00E-05	109.49	440.809	5.00E-05
S000000687	KIN82	64.8765	131.894	5.00E-05	37.1676	123.367	5.00E-05
S000002207	KNH1	114.184	33.9961	5.00E-05	92.0496	14.1129	5.00E-05
S000005076	KRE33	15.2686	5.64704	5.00E-05	9.11685	3.15409	5.00E-05
S000005977	LCL1	69.9854	157.69	5.00E-05	47.5213	133.488	5.00E-05
S000000929	LCP5	18.3427	8.75239	5.00E-05	10.6634	4.79931	5.00E-05
S000000016	LDS1	3.3594	1.53677	0.0035	8.71036	1.70564	5.00E-05
S000005634	LEU9	17.9026	8.41391	5.00E-05			
S000002399	LRG1	6.7562	2.8127	5.00E-05	6.68762	2.47207	5.00E-05
S000000023	MAK16	48.4033	10.5706	5.00E-05	39.1855	7.18658	5.00E-05
S000002467	MAK21	24.2665	10.985	5.00E-05	17.1973	8.21625	5.00E-05
S000003521	MAL11	51.892	105.728	5.00E-05	36.9655	99.2637	5.00E-05
S000003524	MAL12	4.62056	11.541	5.00E-05	2.04916	14.6957	5.00E-05
S000000503	MAL32	1.73687	5.12534	5.00E-05	2.04595	5.13661	5.00E-05
S000007253	MBF1	677.282	2143.05	5.00E-05	418.019	1849.02	5.00E-05
S000000758	MCM3	24.8265	8.63071	5.00E-05	25.506	7.01939	5.00E-05
S000001878	MDJ1	123.148	429.795	5.00E-05	61.3693	437.208	5.00E-05
S000006287	MDM36	105.575	36.0797	5.00E-05	100.458	36.9315	5.00E-05
S000005154	MER1	4.12644	8.37133	0.00035			
S000001484	MET14	13.4569	32.5531	5.00E-05			
S000004294	MET17	13.83	212.722	5.00E-05	14.6252	197.644	5.00E-05
S000001390	MET18	14.2374	5.81586	5.00E-05	12.5698	5.85104	5.00E-05
S000005221	MET2	35.4538	76.2446	5.00E-05	32.6673	67.4231	5.00E-05
S000002661	MET32	15.5467	36.7973	5.00E-05	13.6022	35.1099	5.00E-05
S000000893	MET6	72.6935	149.766	0.0001	54.2453	119.244	5.00E-05
S000006090	MEX67	35.8046	72.2326	5.00E-05	30.625	70.658	5.00E-05
S000006108	MF(ALPHA)1	3192.32	1268.92	5.00E-05			
S000003057	MF(ALPHA)2	16.5822	43.3689	5.00E-05	16.1831	49.101	5.00E-05
S000002392	MFG1	22.5399	49.7626	5.00E-05			
S000003481	MGA1	5.92888	84.3451	5.00E-05	7.73613	98.0943	5.00E-05
S000001472	MGA2	22.6488	50.7685	5.00E-05			
S000005162	MGS1	15.6555	5.54488	5.00E-05	17.8152	5.22557	5.00E-05
S000003985	MHT1	29.4194	73.9614	5.00E-05	24.2556	68.4892	5.00E-05
S000003003	MIG1	45.0012	99.4848	5.00E-05	23.3758	49.6497	5.00E-05
S000007618	MIM2	66.3873	189.103	5.00E-05			
S000005018	MLF3	116.789	265.902	5.00E-05			
S000005061	MLS1	1247.04	623.107	0.00285	3130.43	538.513	5.00E-05
S000003984	MMP1	33.6999	90.3583	5.00E-05	22.3592	76.443	5.00E-05
S000003151	MND1	4.85733	10.704	0.00015			
S000000803	MNN1	28.045	9.68135	5.00E-05	34.2418	8.15886	5.00E-05
S000001859	MOB2	25.1107	11.9749	5.00E-05	21.9122	9.44511	5.00E-05
S000001205	MPC2	665.089	1891.38	5.00E-05	779.344	1570.71	5.00E-05
S000003475	MPC3	569.857	1490.74	5.00E-05	408.814	968.353	5.00E-05
S000005814	MPD1	37.1593	83.8883	5.00E-05			
S000002237	MRK1	96.2431	266.99	5.00E-05	47.3053	268.003	5.00E-05
S000005727	MRM1	58.5743	25.1356	5.00E-05			
S000001785	MSA2	24.022	11.9334	5.00E-05	47.8647	11.1487	5.00E-05
S000004597	MSC1	823.588	1931.05	0.00315	644.317	1486.13	0.00075
S000005450	MSH2	5.52477	2.31984	5.00E-05	12.0268	1.93405	5.00E-05
S000000399	MSI1	6.70357	3.29663	0.0003	5.24299	2.1599	5.00E-05
S000001545	MSN4	122.926	61.348	5.00E-05			
S000002685	MTH1	77.4678	158.509	5.00E-05			
S000003205	MTO1	30.3088	9.58189	5.00E-05			
S000003586	MTR4	25.331	9.63754	5.00E-05	16.8647	5.87537	5.00E-05
S000003287	MUP1	52.5294	214.253	5.00E-05	41.5741	155.891	5.00E-05
S000001028	MUP3	5.52491	31.851	5.00E-05	9.50017	27.4178	5.00E-05
S000000844	MXR1	83.6511	272.786	5.00E-05	74.1645	237.736	5.00E-05
S000006353	NCE102	2441.86	6356.64	0.00015	891.151	2948.65	5.00E-05
S000000120	NCL1	30.2331	12.2856	5.00E-05	22.2728	9.84706	5.00E-05
S000005464	NDJ1	8.6809	26.8646	5.00E-05	3.03989	29.0528	5.00E-05
S000006147	NEW1	33.2859	10.1557	5.00E-05	24.166	6.8058	5.00E-05
S000004926	NIP1	54.7283	22.154	5.00E-05	39.2515	13.7938	5.00E-05

S000006095	NIP100	20.0232	9.87727	5.00E-05	20.5996	10.003	5.00E-05
S000006132	NIP7	70.1231	28.7328	5.00E-05			
S000001426	NIT1	27.6155	58.471	5.00E-05			
S000002791	NKP1	23.8419	11.4711	5.00E-05	29.3965	11.4363	5.00E-05
S000003873	NNF1	50.5135	22.7597	5.00E-05	69.6975	26.9129	5.00E-05
S000003992	NOC3	18.1014	8.38755	5.00E-05	16.1883	6.84705	5.00E-05
S000006014	NOG1	56.529	26.7446	5.00E-05	33.5067	14.0788	5.00E-05
S000005336	NOG2	45.096	18.9203	5.00E-05	28.7149	11.6285	5.00E-05
S000002172	NOP1	105.985	52.0395	5.00E-05	57.8113	26.599	5.00E-05
S000005401	NOP12	39.7361	16.3833	5.00E-05	29.591	11.7982	5.00E-05
S000005119	NOP13	35.5818	14.5629	5.00E-05			
S000002307	NOP14	29.7324	13.3301	5.00E-05	22.8996	9.81193	5.00E-05
S000005054	NOP15	86.8883	42.871	5.00E-05	69.4571	30.7187	5.00E-05
S000005837	NOP58	58.8772	27.5165	5.00E-05	45.944	18.3079	5.00E-05
S000002326	NRP1	15.3798	6.66909	5.00E-05	11.3121	5.40001	5.00E-05
S000000928	NSA2	58.1265	27.2507	5.00E-05	42.8054	17.236	5.00E-05
S000002408	NTH1	222.803	465.214	0.0002	177.254	449.294	5.00E-05
S000003744	NUC1	39.0463	17.3403	5.00E-05	31.8156	11.8432	5.00E-05
S000003006	OCH1	115.022	45.5023	5.00E-05	119.083	46.1648	5.00E-05
S000003023	OLE1	986.232	4357.04	5.00E-05			
S000005392	OPI10	83.1977	418.574	5.00E-05	50.1825	394.528	5.00E-05
S000004044	OSW2	5.54077	11.5445	5.00E-05			
S000006092	OYE3	66.4708	321.526	5.00E-05	40.659	336.798	5.00E-05
S000005795	PAC1	8.40274	4.05154	0.0001			
S000003230	PAU11	2.32029	6.24725	0.00805	2.04075	4.8953	0.01565
S000004141	PCD1	43.97	102.566	5.00E-05			
S000005233	PCL1	12.2201	2.58312	5.00E-05	34.9575	2.7047	5.00E-05
S000001113	PCL5	185.599	466.573	5.00E-05	140.968	353.99	5.00E-05
S000006206	PDH1	222.624	64.4133	5.00E-05	246.107	39.9525	5.00E-05
S000005175	PDR16	59.5999	170.397	5.00E-05	45.5575	122.454	5.00E-05
S000005679	PDR5	22.117	115.381	5.00E-05	17.3263	87.3533	5.00E-05
S000004844	PEP5	8.87705	4.36426	5.00E-05	9.02065	4.37269	5.00E-05
S000004054	PER33	41.7302	225.368	5.00E-05	35.5319	171.202	5.00E-05
S000004870	PET111	24.6946	7.82246	5.00E-05			
S000005496	PFK27	5.71923	21.2296	5.00E-05	5.83614	15.4152	5.00E-05
S000004711	PGM2	185.179	695.09	5.00E-05	236.304	752.414	5.00E-05
S000001526	PHD1	84.545	203.402	5.00E-05	31.2542	120.01	5.00E-05
S000002689	PHM6	37.4029	3.85704	5.00E-05	46.67	3.70643	5.00E-05
S000005444	PHM7	34.9475	16.2479	5.00E-05	46.6735	9.40102	5.00E-05
S000000296	PHO3	47.3695	14.3579	5.00E-05	42.498	14.5494	5.00E-05
S000005913	PHR1	28.1685	74.3051	5.00E-05	31.6953	82.1752	5.00E-05
S000000855	PIC2	406.894	852.013	0.0002	186.655	699.056	5.00E-05
S000006358	PIN3	143.707	631.518	5.00E-05	171.682	638.042	5.00E-05
S000001646	PIR3	654.545	271.696	5.00E-05	751.04	229.563	5.00E-05
S000003696	PIR5	12.2928	2.79294	5.00E-05	13.8121	2.63897	5.00E-05
S000006317	PIS1	107.372	623.936	5.00E-05	83.4908	509.906	5.00E-05
S000004610	PLB1	254.049	538.54	0.0001			
S000005687	PNS1	65.4663	157.038	0.00015	25.8189	103.668	5.00E-05
S000005046	POL1	9.89719	4.11973	5.00E-05	17.6064	3.959	5.00E-05
S000003804	POL32	9.0061	2.92513	5.00E-05	9.54728	1.73123	5.00E-05
S000005501	PPM2	8.00417	3.2584	5.00E-05	5.19701	2.44804	5.00E-05
S000003355	PPT1	13.3269	5.09495	5.00E-05	10.3258	2.59034	5.00E-05
S000003021	PRM8	70.4623	158.064	5.00E-05	67.1984	144.151	5.00E-05
S000003088	PRP43	28.2009	11.2761	5.00E-05	20.8591	8.33476	5.00E-05
S000004009	PSR2	84.2625	32.0993	5.00E-05	67.3349	25.5013	5.00E-05
S000002462	PST1	517.193	244.263	5.00E-05	568.435	179.919	5.00E-05
S000001801	PTR2	20.1587	9.91542	5.00E-05	19.2803	5.59413	5.00E-05
S000002904	PUF6	45.0845	19.075	5.00E-05	34.6619	13.7203	5.00E-05
S000006133	PUS1	14.2827	5.21847	5.00E-05	16.2742	3.10543	5.00E-05
S000005769	PUS7	17.9359	8.84863	5.00E-05			
S000005875	PUT4	153.139	64.0407	5.00E-05	360.043	44.666	5.00E-05
S000004186	PWP1	30.6414	12.747	5.00E-05	25.9546	8.1664	5.00E-05
S000000653	PWP2	21.3715	7.07459	5.00E-05	13.977	3.94731	5.00E-05
S000003512	PXR1	89.5109	256.625	5.00E-05	72.565	247.525	5.00E-05
S000003030	PYC1	1011.36	464.219	0.0009			
S000001383	QDR2	15.059	45.0682	5.00E-05	16.0134	48.6682	5.00E-05

S000000318	RAD16	20.0256	40.1226	5.00E-05	14.6127	32.1909	5.00E-05
S000004022	RAD5	12.5947	5.66734	5.00E-05	15.8364	5.44783	5.00E-05
S000006074	RAD53	3.11188	1.41278	5.00E-05	8.01392	1.58096	5.00E-05
S000005746	RCN2	404.916	841.61	5.00E-05	331.901	666.447	5.00E-05
S000000471	REI1	48.1867	22.8711	5.00E-05			
S000006088	REV3	14.6737	7.06608	5.00E-05	14.5578	7.17216	5.00E-05
S000000869	RGI1	1228.72	4813.18	5.00E-05	858.839	5019.73	5.00E-05
S000000460	RIB5	280.313	633.392	5.00E-05	230.458	553.815	5.00E-05
S000000357	RIB7	43.2022	21.0713	5.00E-05			
S000004029	RIC1	14.3791	7.04222	5.00E-05	13.9685	6.27783	5.00E-05
S000001240	RIX1	14.2557	6.31291	5.00E-05			
S000003957	RIX7	7.42336	2.01343	5.00E-05	5.55231	1.36909	5.00E-05
S000005621	RKI1	194.442	94.4418	5.00E-05	217.855	92.501	5.00E-05
S000006222	RLF2	16.5216	6.1832	5.00E-05	30.5414	6.22117	5.00E-05
S000002498	RLI1	31.4512	14.1289	5.00E-05	24.2523	11.4592	5.00E-05
S000005945	RMI1	118.298	39.1396	5.00E-05	119.638	33.3109	5.00E-05
S000003219	RMR1	56.3411	115.424	5.00E-05	48.3542	105.234	5.00E-05
S000000872	RNR1	9.56814	4.28982	5.00E-05	25.5168	3.00794	5.00E-05
S000004852	RNT1	15.6453	6.17299	5.00E-05	14.6756	4.54513	5.00E-05
S000003139	ROK1	25.9919	9.41305	5.00E-05	18.9463	7.28444	5.00E-05
S000003824	RPA12	27.4907	12.7165	0.00025	22.5759	6.50844	5.00E-05
S000006214	RPA135	31.2477	12.422	5.00E-05	20.8729	7.79039	5.00E-05
S000003684	RPA34	60.8267	24.7749	5.00E-05	49.6304	21.8401	5.00E-05
S000005867	RPA43	14.4659	4.70102	5.00E-05	8.92083	3.96731	5.00E-05
S000005192	RPA49	24.8865	5.51586	5.00E-05	17.9171	4.06187	5.00E-05
S000005057	RPC19	59.0473	29.2804	5.00E-05	35.6391	17.6213	0.0001
S000005095	RPC31	59.5542	28.8814	5.00E-05	57.0269	26.5119	5.00E-05
S000001789	RPF2	56.9687	23.7232	5.00E-05	40.38	18.902	5.00E-05
S000001381	RPI1	26.5775	12.6002	5.00E-05	26.7623	11.7799	5.00E-05
S000002826	RPL12B	493.027	204.838	5.00E-05	380.342	143.406	5.00E-05
S000002240	RPL13A	236.996	87.6432	5.00E-05	147.469	66.202	5.00E-05
S000001489	RPL14A	373.898	155.729	5.00E-05	289.393	111.408	5.00E-05
S000003713	RPL17B	284.091	120.904	5.00E-05	208.587	92.6891	5.00E-05
S000005245	RPL18B	128.665	52.0637	5.00E-05	129.761	39.4382	5.00E-05
S000006000	RPL21B	427.555	133.657	5.00E-05	310.46	98.6525	5.00E-05
S000004051	RPL22A	570.224	262.675	5.00E-05	368.854	163.664	5.00E-05
S000006436	RPL22B	86.7937	27.305	5.00E-05	47.652	20.891	5.00E-05
S000003266	RPL26B	511.881	239.037	5.00E-05	387.214	186.218	5.00E-05
S000002879	RPL27B	445.265	184.278	5.00E-05	299.002	107.586	5.00E-05
S000004440	RPL6B	114.959	54.3184	5.00E-05	76.5397	36.4594	5.00E-05
S000006119	RPL7B	116.439	42.7505	5.00E-05	71.0593	31.9333	5.00E-05
S000001025	RPL8A	487.248	200.79	5.00E-05	313.224	153.59	5.00E-05
S000003968	RPL8B	431.068	206.212	5.00E-05			
S000001454	RPR2	56.7702	22.5981	5.00E-05			
S000003727	RPS14B	333.838	165.304	5.00E-05	238.458	118.87	5.00E-05
S000002241	RPS16B	581.591	275.136	5.00E-05			
S000004488	RPS18B	517.513	235.713	5.00E-05	390.049	184.022	5.00E-05
S000005481	RPS19A	477.822	205.597	5.00E-05	375.81	159.045	5.00E-05
S000004528	RPS1B	591.041	283.484	5.00E-05			
S000003091	RPS2	742.783	281.984	5.00E-05	463.275	217.331	5.00E-05
S000003726	RPS22A	356.32	118.766	5.00E-05	268.026	105.853	5.00E-05
S000001246	RPS4B	445.697	214.795	5.00E-05			
S000005622	RPS7A	541.916	214.406	5.00E-05	424.341	168.791	5.00E-05
S000005477	RRI2	31.0717	63.777	5.00E-05			
S000004507	RRN11	14.239	3.93954	5.00E-05	11.8951	2.9405	5.00E-05
S000004131	RRN5	11.8519	23.7924	5.00E-05			
S000005933	RRP12	18.8805	7.26453	5.00E-05	12.7504	4.08701	5.00E-05
S000001107	RRP3	42.9001	14.8204	5.00E-05	31.0457	11.5868	5.00E-05
S000004842	RRP5	24.4501	8.63418	5.00E-05	15.346	6.14133	5.00E-05
S000006341	RRP9	19.4879	9.20102	5.00E-05	18.5358	5.96736	5.00E-05
S000000868	RRT13	27.9085	82.6568	5.00E-05	17.4428	78.8312	5.00E-05
S000000668	RSA4	9.48986	2.81032	5.00E-05	7.42858	1.67211	5.00E-05
S000005575	RSB1	33.8823	91.9758	5.00E-05	32.6615	77.7188	5.00E-05
S000001638	RSM22	37.6226	15.8818	5.00E-05			
S000001129	RTC3	921.053	2988.49	5.00E-05	467.588	2935.58	5.00E-05
S000002363	RTN2	447.342	1201.91	0.0003	251.467	881.849	5.00E-05

S000003393	RTS3	96.3442	585.559	5.00E-05	121.214	443.899	5.00E-05
S000006104	RTT10	10.3081	4.19871	5.00E-05	8.80314	3.00435	5.00E-05
S000000602	RVS161	222.371	512.151	5.00E-05			
S000002536	SAC6	203.639	537.322	5.00E-05	174.473	512.351	5.00E-05
S000004170	SAM1	7.15065	181.968	5.00E-05	7.25336	135.092	5.00E-05
S000002910	SAM2	35.2592	165.005	5.00E-05	23.7008	143.641	5.00E-05
S000003198	SAP4	3.95441	8.03414	5.00E-05	2.92694	7.66083	5.00E-05
S000003094	SCS3	26.5813	58.2261	5.00E-05			
S000003511	SCW4	103.174	290.455	5.00E-05			
S000000200	SEA4	12.8159	6.37521	5.00E-05			
S000005780	SEC63	19.6636	9.0689	5.00E-05	23.5427	7.66216	5.00E-05
S000002484	SED1	6363.82	2966.04	0.00075	3941.31	1786.51	0.00025
S000000066	SEN34	10.1616	4.35474	5.00E-05	27.2715	4.57259	5.00E-05
S000000062	SEO1	10.1137	28.4991	5.00E-05			
S000003440	SER2	4.64842	2.24382	0.0009	9.79439	2.37166	5.00E-05
S000000883	SER3	188.274	66.1986	5.00E-05			
S000001534	SFK1	52.3418	152.069	5.00E-05	45.3088	126.779	5.00E-05
S000001361	SGA1	12.4188	26.4636	5.00E-05			
S000004724	SHH3	399.014	151.896	5.00E-05	476.842	119.837	5.00E-05
S000004154	SHH4	228.275	77.8915	5.00E-05	187.718	53.6017	5.00E-05
S000004787	SIP18	25521.7	10251.3	5.00E-05			
S000004952	SIS1	109.341	565.303	5.00E-05	94.6495	556.154	5.00E-05
S000004829	SKY1	39.1488	88.0775	5.00E-05			
S000002923	SLF1	32.5698	12.877	5.00E-05			
S000004129	SLS1	17.3272	6.02441	5.00E-05			
S000005854	SNC2	484.047	1202.46	5.00E-05			
S000002480	SNF11	123.82	280.771	5.00E-05	71.7685	236.789	5.00E-05
S000003429	SNG1	27.803	2465.87	5.00E-05	22.1638	1760.11	5.00E-05
S000002418	SNQ2	36.2303	2675.26	5.00E-05	28.8996	2166.33	5.00E-05
S000006499	snR14	18.4911	53.4197	0.0237	23.3885	111.209	0.0012
S000081374	snR80	0	6.79246	0.02395			
S000028467	snR82	73.7933	164.606	5.00E-05			
S000003934	SOF1	29.7247	8.47902	5.00E-05	21.3192	5.61469	5.00E-05
S000001206	SOL3	19.0382	47.796	5.00E-05			
S000003480	SOL4	507.105	1372.11	5.00E-05	325.238	1045.38	5.00E-05
S000000559	SPB1	17.2043	4.38038	5.00E-05	14.518	3.02525	5.00E-05
S000004305	SPH1	2.83291	1.35858	0.0007	8.65059	1.43875	5.00E-05
S000000952	SPI1	5286.13	20732.3	5.00E-05	2162.12	14795.3	5.00E-05
S000001178	SPL2	97.4815	323.756	5.00E-05	89.1363	281.452	5.00E-05
S000006051	SPO19	5.34838	1.40295	0.0001	12.4876	2.39225	5.00E-05
S000028425	SPO24	6834.37	18067.2	5.00E-05			
S000000848	SPO73	115.592	49.2243	5.00E-05	104.301	32.7218	5.00E-05
S000002291	SRF1	54.7122	20.9752	5.00E-05	44.9244	18.5166	5.00E-05
S000029010	SRG1	395.945	195.258	0.00405	289.224	137.032	0.0013
S000005954	SRL4	2.09388	0.72523	0.00485	5.24149	1.08432	5.00E-05
S000001701	SRY1	50.7554	136.963	5.00E-05	39.7896	129.973	5.00E-05
S000003947	SSA2	98.5066	223.33	0.00025	50.9011	254.922	5.00E-05
S000000171	SSA3	528.833	252.076	0.0001			
S000000905	SSA4	115.669	613.136	5.00E-05	65.9728	1021.62	5.00E-05
S000002388	SSB1	213.84	93.3427	5.00E-05	155.076	66.1746	5.00E-05
S000006027	SSE1	346.915	862.74	5.00E-05	169.673	731.885	5.00E-05
S000000373	SSE2	180.256	590.904	5.00E-05	128.804	574.016	5.00E-05
S000001108	SSF1	28.0278	7.07404	5.00E-05	20.2138	5.92685	5.00E-05
S000001227	SSP1	7.94794	3.67037	5.00E-05	12.631	3.0942	5.00E-05
S000001555	STB6	3.32346	7.63293	5.00E-05	3.03402	7.83041	5.00E-05
S000003240	STF2	3607.32	9148.18	0.00015	2543.86	8178.4	5.00E-05
S000002944	STL1	103.764	23.5857	5.00E-05	111.059	19.685	5.00E-05
S000003152	STR3	7.41503	47.9499	5.00E-05	11.29	33.3703	5.00E-05
S000001424	SUC2	117.516	383.806	5.00E-05	58.616	416.392	5.00E-05
S000002705	SUR2	76.172	196.523	5.00E-05			
S000004516	SUR7	38.0137	101.218	5.00E-05	37.1286	100.198	5.00E-05
S000003130	SUT1	32.2566	14.6645	5.00E-05			
S000000009	SWC3	17.6934	7.52107	5.00E-05	14.3336	6.40245	5.00E-05
S000004241	SYM1	52.0053	127.848	5.00E-05	65.4086	141.464	5.00E-05
S000002221	SYO1	16.608	7.35112	5.00E-05	9.58022	4.3519	5.00E-05
S000003807	TAH11	28.1102	80.4834	5.00E-05	20.2645	73.3473	5.00E-05

S000000273	TAT1	126.133	51.6732	5.00E-05	129.901	44.3374	5.00E-05
S000005380	TAT2	86.5965	40.6238	5.00E-05			
S000003437	TDA10	45.3027	91.7596	5.00E-05	20.1348	78.4078	5.00E-05
S000003877	TDA4	19.7325	43.4228	5.00E-05			
S000003588	TDH1	2585.92	6308.79	0.0005			
S000000287	TEC1	58.1313	122.158	5.00E-05	28.0128	125.67	5.00E-05
S000001623	TGL1	42.6045	97.2263	5.00E-05	37.5003	76.0236	5.00E-05
S000003394	TIF4631	50.8142	23.2496	5.00E-05	37.27	17.1861	5.00E-05
S000000813	TIR1	9.28877	70.9389	5.00E-05			
S000006657	TLC1	11.4861	42.2731	5.00E-05			
S000004319	TMA10	6932.05	18579.4	5.00E-05	2853.34	13259.1	5.00E-05
S000005217	TOF1	3.46937	1.71596	5.00E-05	5.21461	1.85793	5.00E-05
S000003147	TOS3	2.86945	6.01698	5.00E-05			
S000003951	TPO1	15.332	39.5111	5.00E-05	13.1974	33.9216	5.00E-05
S000000330	TPS1	382.143	963.39	0.0001	329.538	950.684	5.00E-05
S000002481	TPS2	108.964	306.546	5.00E-05	82.8136	325.501	5.00E-05
S000004874	TPS3	19.5984	53.8963	5.00E-05	18.0507	65.6331	5.00E-05
S000003623	TRL1	6.7772	3.1354	5.00E-05	7.14084	3.20678	5.00E-05
S000002270	TRM3	9.9269	4.85937	5.00E-05			
S000002360	TRM8	55.892	21.62	5.00E-05	35.4088	17.0048	5.00E-05
S000002762	TRP4	21.1205	9.57498	5.00E-05	21.4958	8.00962	5.00E-05
S000002761	TRR1	124.767	267.224	5.00E-05			
S000003441	TRX2	1432.92	3017.23	5.00E-05			
S000002861	TSA2	183.732	742.154	5.00E-05	131.932	630.824	5.00E-05
S000004566	TSL1	99.6255	318.274	5.00E-05	94.0294	321.646	5.00E-05
S000002218	TSR1	24.5351	11.9556	5.00E-05			
S000004427	TSR2	23.03	10.3687	5.00E-05	22.083	7.78963	5.00E-05
S000004550	TUB1	71.8781	152.702	5.00E-05			
S000000286	UBC4	478.589	972.962	5.00E-05	364.259	847.732	5.00E-05
S000001806	UBP11	22.4936	55.7715	5.00E-05	13.4624	51.1445	5.00E-05
S000004214	UCC1	45.1422	95.2393	5.00E-05	25.8721	68.2302	5.00E-05
S000001518	UGP1	176.738	466.925	5.00E-05	194.558	518.15	5.00E-05
S000004158	UPS2	170.904	369.302	5.00E-05	84.5037	338.471	5.00E-05
S000000135	URA7	18.1565	3.64158	5.00E-05	13.0591	2.25332	5.00E-05
S000003864	URA8	220.368	470.116	5.00E-05	179.463	391.834	5.00E-05
S000001497	URB1	8.90672	3.75421	5.00E-05	6.35471	2.84083	5.00E-05
S000003802	URB2	8.63429	3.0391	5.00E-05	5.8594	2.30253	5.00E-05
S000006151	USV1	210.362	434.709	5.00E-05	101.732	385.163	5.00E-05
S000003645	UTP10	14.8356	6.04376	5.00E-05	10.0198	4.77977	5.00E-05
S000004212	UTP13	22.1381	7.69962	5.00E-05	14.9378	6.05148	5.00E-05
S000004558	UTP14	31.1045	11.8065	5.00E-05	20.8816	9.0263	5.00E-05
S000004699	UTP15	18.3077	6.37752	5.00E-05	14.6999	4.26152	5.00E-05
S000004401	UTP21	16.7113	5.671	5.00E-05	12.2091	4.81566	5.00E-05
S000001353	UTP25	20.7517	8.69843	5.00E-05	14.1878	5.87946	5.00E-05
S000002732	UTP4	23.3011	6.50267	5.00E-05	17.1908	4.46357	5.00E-05
S000002857	UTP6	15.1472	6.37449	5.00E-05	12.6065	4.06159	5.00E-05
S000003360	UTP8	17.0022	5.85318	5.00E-05	12.7435	3.95099	5.00E-05
S000001318	VHR1	28.0081	133.16	5.00E-05	25.9354	93.9586	5.00E-05
S000003297	VHT1	30.5277	9.71932	5.00E-05	21.3327	10.1845	5.00E-05
S000003963	VPS13	26.9085	55.7806	5.00E-05	17.258	52.6048	5.00E-05
S000005886	VTS1	13.1689	4.72334	5.00E-05	6.96878	2.74214	5.00E-05
S000003426	XKS1	68.724	166.732	5.00E-05	65.0917	180.104	5.00E-05
S000006173	YAH1	84.8013	37.0261	5.00E-05			
S000003473	YAP1802	30.3658	65.1994	5.00E-05	19.7592	67.3544	5.00E-05
S000001457	YAP5	41.5329	98.0524	5.00E-05	27.1479	77.2402	5.00E-05
S000000826	YAT2	286.09	135.688	5.00E-05	455.573	130.926	5.00E-05
S000002147	YBL005W-B	7.2352	14.4934	0.0002	5.04126	13.5119	5.00E-05
S000000177	YBL081W	17.8957	6.55085	5.00E-05	13.5904	4.98373	5.00E-05
S000000182	YBL086C	86.6122	191.974	5.00E-05	55.9493	165.83	5.00E-05
S000000260	YBR056W	157.848	319.764	0.00015			
S000000300	YBR096W	30.1945	67.9404	5.00E-05	30.2612	66.7844	5.00E-05
S000000342	YBR138C	11.922	25.6228	5.00E-05	11.6614	23.8921	5.00E-05
S000000489	YBR285W	50.736	111.608	5.00E-05	40.139	97.8416	5.00E-05
S000003978	YCT1	39.8339	124.438	5.00E-05	36.1994	78.2139	5.00E-05
S000005008	YDJ1	97.6358	253.604	5.00E-05	63.6708	216.625	5.00E-05
S000002345	YDL186W	4.43748	9.39	0.00015			

S000002541	YDR134C	2359	8210.91	5.00E-05			
S000007409	YDR210W-C	2.26486	7.60795	0.00285			
S000002656	YDR248C	64.2627	195.12	5.00E-05	47.064	163.582	5.00E-05
S000000767	YEF1	20.2542	48.4979	5.00E-05	19.0798	39.6178	5.00E-05
S000003935	YEH1	5.89977	2.69878	5.00E-05	5.64995	2.64549	5.00E-05
S000007226	YER039C-A	34.4183	72.3834	0.0006			
S000000886	YER084W	39.6895	10.4351	5.00E-05	29.4696	6.50821	5.00E-05
S000000936	YER134C	89.1743	204.704	5.00E-05	79.9806	174.339	5.00E-05
S000001843	YFL051C	18.1994	47.5723	5.00E-05	11.0592	45.407	5.00E-05
S000001840	YFL054C	37.9699	92.0309	5.00E-05	11.8549	74.2632	5.00E-05
S000003267	YGR035C	10.9276	658.059	5.00E-05	7.6656	422.94	5.00E-05
S000028827	YGR035W-A	22.7973	63.8897	5.00E-05	26.0659	73.4231	0.0001
S000003298	YGR066C	11.4	27.3704	5.00E-05	9.37403	25.9768	5.00E-05
S000003299	YGR067C	155.471	26.9487	5.00E-05	186.522	22.5461	5.00E-05
S000029726	YGR161W-C	187.07	793.107	5.00E-05	183.959	586.761	5.00E-05
S000001253	YHR210C	2.48482	5.31384	0.00035	2.56538	5.99496	5.00E-05
S000001268	YIA6	27.0831	7.4322	5.00E-05	22.0617	6.57927	5.00E-05
S000001427	YIL165C	28.0761	66.7634	5.00E-05	25.0981	63.8166	5.00E-05
S000001428	YIL166C	9.13373	21.6076	5.00E-05			
S000001453	YIR014W	28.9794	11.1996	5.00E-05			
S000003581	YJL045W	103.682	48.9459	5.00E-05	255.04	48.5505	5.00E-05
S000003680	YJL144W	401.678	950.903	5.00E-05	224.311	860.877	5.00E-05
S000003717	YJL181W	11.1425	2.78098	5.00E-05	10.502	3.08377	5.00E-05
S000003749	YJL213W	16.9284	40.4152	5.00E-05	10.665	37.2564	5.00E-05
S000003857	YJR096W	444.813	1409.92	5.00E-05	366.445	1242.82	5.00E-05
S000003903	YJR142W	44.6698	105.08	5.00E-05	45.7321	98.7388	5.00E-05
S000028524	YKL068W-A	48.586	100.227	0.0002			
S000003979	YLL056C	31.5541	1761.91	5.00E-05	35.9681	1347.23	5.00E-05
S000007225	YLR035C-A	0.841444	3.68526	5.00E-05	0.648652	1.86402	5.00E-05
S000004036	YLR046C	28.7813	163.244	5.00E-05	20.5354	82.6531	5.00E-05
S000004039	YLR049C	24.8812	56.5016	5.00E-05			
S000004167	YLR177W	25.8417	89.6173	5.00E-05	18.336	89.4019	5.00E-05
S000004169	YLR179C	70.8851	187.815	5.00E-05	70.7937	170.029	5.00E-05
S000007377	YLR256W-A	3.99642	1.95106	0.00155			
S000004288	YLR297W	123.488	268.417	5.00E-05	114.133	254.888	5.00E-05
S000007620	YLR363W-A	111.622	45.3859	5.00E-05	83.4961	38.1912	5.00E-05
S000028572	YLR412C-A	0	2.94131	0.00285			
S000004411	YLR419W	11.3833	4.32776	5.00E-05	8.98418	3.85601	5.00E-05
S000004438	YLR446W	11.5029	26.463	5.00E-05	11.1222	26.152	5.00E-05
S000004502	YMD8	19.633	7.22609	5.00E-05	30.0437	6.30753	5.00E-05
S000004501	YML037C	5.9669	1.71216	5.00E-05	9.59814	2.39199	5.00E-05
S000004600	YML131W	137.802	286.995	5.00E-05	98.0768	254.913	5.00E-05
S000004696	YMR090W	537.078	1093.05	0.0002	451.555	917.122	0.0001
S000004708	YMR102C	4.59417	17.3126	5.00E-05			
S000005003	YNL058C	44.334	99.0675	5.00E-05	25.1159	78.3084	5.00E-05
S000005297	YNR014W	43.5077	106.253	5.00E-05	14.0506	103.327	5.00E-05
S000005354	YNR071C	7.6562	28.515	5.00E-05	5.58959	27.6355	5.00E-05
S000005356	YNR073C	6.87365	14.8649	5.00E-05	3.68124	19.0484	5.00E-05
S000005374	YOL014W	6.76842	25.9336	5.00E-05			
S000005379	YOL019W	26.1458	11.8805	5.00E-05	31.3222	10.5025	5.00E-05
S000005513	YOL153C	77.4708	182.022	5.00E-05	56.5679	182.69	5.00E-05
S000003513	YOR1	35.6511	127.338	5.00E-05	21.5577	82.0944	5.00E-05
S000005657	YOR131C	73.6438	149.992	5.00E-05			
S000005865	YOR338W	41.3869	345.399	5.00E-05	58.9536	245.884	5.00E-05
S000028586	YOR376W-A	43.9752	112.127	0.0096			
S000005914	YOR387C	6.97072	14.3335	0.0005			
S000004710	YPK2	85.7684	186.897	5.00E-05			
S000000232	YPK3	15.9676	7.56922	5.00E-05	18.9156	6.26242	5.00E-05
S000006009	YPL088W	81.1539	217.523	5.00E-05	52.5482	190.835	5.00E-05
S000006168	YPL247C	87.4328	235.365	5.00E-05	36.4747	246.887	5.00E-05
S000003430	YPP1	21.2517	256.13	5.00E-05	20.81	193.927	5.00E-05
S000006231	YPR027C	64.4411	158.628	5.00E-05	38.9963	141.16	5.00E-05
S000006300	YPR096C	1.50316	0	0.00015			
S000113589	YPR145C-A	18.5119	181.46	5.00E-05			
S000003228	YPS5	25.317	52.2787	5.00E-05			
S000005037	YPT53	87.3854	177.942	5.00E-05			

S000005688	YRR1	31.9266	89.0518	5.00E-05	31.9236	71.1598	5.00E-05
S000001059	YSC83	59.293	127.75	5.00E-05	44.7485	110.295	5.00E-05
S000001058	YSC84	112.712	270.867	5.00E-05	82.5303	280.837	5.00E-05
S000004577	ZDS2	11.0671	3.68309	5.00E-05	14.9622	3.55109	5.00E-05
S000001842	ZNF1	23.066	56.2003	5.00E-05	16.28	57.9382	5.00E-05
S000003443	ZPR1	42.1113	143.617	5.00E-05	24.9342	211.419	5.00E-05
S000001595	ABF1				35.0392	16.036	5.00E-05
S000000684	ABP1				66.6631	136.407	5.00E-05
S000000111	ACH1				2478.56	1010.82	5.00E-05
S000006188	ACM1				19.3585	5.99667	5.00E-05
S000003736	ACO2				8.94216	4.073	5.00E-05
S000004143	ACS2				217.463	61.475	5.00E-05
S000002856	ADA2				9.93631	21.0936	5.00E-05
S000004727	ADE17				129.274	28.5814	5.00E-05
S000005654	ADE2				83.476	41.2575	5.00E-05
S000003203	ADE5%2C7				64.3607	25.7658	5.00E-05
S000003293	ADE6				38.6213	19.035	5.00E-05
S000004918	ADH2				2456.91	73.9881	5.00E-05
S000000604	ADP1				44.4761	91.2552	5.00E-05
S000002492	ADY2				967.969	190.149	5.00E-05
S000000603	AFR1				33.162	67.9493	5.00E-05
S000000530	AGP1				323.031	90.5263	5.00E-05
S000002622	AHA1				254.918	609.565	5.00E-05
S000005549	AHC1				67.1519	142.733	5.00E-05
S000007261	AI1				39.3909	12.1599	5.00E-05
S000007262	AI2				28.2984	7.98131	0.0001
S000003667	AIM23				44.589	104.049	5.00E-05
S000001520	AIM26				3.91131	9.96621	0.00115
S000006079	AIM44				13.9511	29.2034	5.00E-05
S000001242	AIM46				172.626	357.976	5.00E-05
S000004698	AIP1				57.5028	119.091	5.00E-05
S000000263	AKL1				30.6076	62.4847	5.00E-05
S000005701	ALE1				50.1481	101.254	5.00E-05
S000000274	ALG14				113.262	40.5422	5.00E-05
S000000105	ALK2				16.9162	6.67948	5.00E-05
S000005214	ALP1				28.6917	13.4587	5.00E-05
S000004079	ALT1				33.5171	106.326	5.00E-05
S000004498	AMD1				27.0541	68.956	5.00E-05
S000000362	AMN1				32.6836	98.1935	5.00E-05
S000001168	ANS1				5.16691	1.15076	0.0002
S000002938	APA2				170.783	368.296	5.00E-05
S000000490	APE3				698.235	2008.12	5.00E-05
S000005009	AQR1				11.7653	5.40238	5.00E-05
S000001324	ARC15				290.318	592.112	5.00E-05
S000005419	ARG1				330.298	146.689	5.00E-05
S000003624	ARG3				60.0479	15.378	5.00E-05
S000001179	ARO9				84.1733	36.526	5.00E-05
S000003651	ASF1				74.0465	31.9417	5.00E-05
S000003409	ATF2				7.53786	3.22984	5.00E-05
S000002792	ATO3				92.3107	10.743	5.00E-05
S000005537	AUS1				7.46196	2.87627	5.00E-05
S000004672	AVO2				33.3948	67.9721	5.00E-05
S000001402	AXL2				22.7196	8.5314	5.00E-05
S000003909	BAT2				582.861	1210.12	0.00035
S000003557	BBC1				52.2141	135.303	5.00E-05
S000006176	BBP1				12.663	6.25764	5.00E-05
S000001295	BCY1				273.187	583.345	0.0001
S000005341	BIO3				12.4732	5.09983	5.00E-05
S000003839	BNA2				98.5062	38.1824	0.02315
S000005177	BNI4				26.4558	9.3894	5.00E-05
S000005110	BNI5				15.2404	6.21169	5.00E-05
S000005213	BSC4				7.05743	14.9373	0.00105
S000005352	BSC5				12.5776	26.3875	5.00E-05
S000005497	BSC6				26.3888	12.3402	5.00E-05
S000000755	BUD16				15.6201	6.54666	5.00E-05
S000004616	BUD22				26.4922	13.2427	5.00E-05

S000002831	CAD1		64.8876	130.76	5.00E-05
S000004893	CAT8		39.6888	90.7138	5.00E-05
S000000335	CCZ1		3.74338	1.62517	5.00E-05
S000004298	CDA1		15.8623	4.65617	5.00E-05
S000004299	CDA2		8.13253	0.306864	5.00E-05
S000000036	CDC19		1298.55	483.166	5.00E-05
S000005600	CDC21		48.4518	7.22454	5.00E-05
S000004301	CDC25		26.9139	12.8113	5.00E-05
S000004093	CDC45		8.53135	2.07735	5.00E-05
S000002284	CDC48		300.371	691.813	0.00015
S000003730	CDC6		5.54394	1.73162	5.00E-05
S000002323	CDC9		21.0866	7.32744	5.00E-05
S000002997	CGR1		45.7097	20.9288	5.00E-05
S000000569	CHA1		639.281	2146.98	5.00E-05
S000000828	CHO1		252.813	509.103	5.00E-05
S000005876	CIN1		15.438	7.28222	5.00E-05
S000006162	CIN2		23.6228	10.8873	5.00E-05
S000000598	CIT2		2575.23	505.941	5.00E-05
S000006205	CIT3		187.311	29.6418	5.00E-05
S000003341	CLB6		3.84414	1.66956	0.0004
S000006177	CLN2		44.4438	19.4753	5.00E-05
S000004857	COA6		243.599	501.056	5.00E-05
S000007270	COB		5.69188	2.76024	0.0028
S000000207	COQ1		29.1338	63.5465	5.00E-05
S000005456	COQ3		36.7883	74.3593	5.00E-05
S000002612	COQ4		161.958	338.768	5.00E-05
S000004191	COQ9		117.474	266.604	5.00E-05
S000003932	COX17		403.007	1052.21	5.00E-05
S000003294	COX18		31.6592	87.7748	5.00E-05
S000001158	COX23		20.2276	48.2421	5.00E-05
S000003793	CPR7		15.1345	6.79429	5.00E-05
S000005626	CRC1		337.051	155.168	5.00E-05
S000003421	CRH1		207.307	82.631	5.00E-05
S000004077	CSF1		7.4668	16.0584	5.00E-05
S000005367	CSI2		35.71	14.7855	5.00E-05
S000004651	CSM3		41.6231	19.9196	5.00E-05
S000002586	CSN9		51.0268	22.5454	5.00E-05
S000001298	CST6		37.4259	77.3487	5.00E-05
S000002664	CTA1		290.491	87.4268	5.00E-05
S000004700	CTF13		10.6535	4.88351	5.00E-05
S000004683	CTF18		20.4308	9.88536	5.00E-05
S000005568	CUE5		148.903	311.263	5.00E-05
S000005099	CUZ1		52.6036	112.781	5.00E-05
S000001956	CWP2		10176.6	4661.17	5.00E-05
S000003387	CYS4		164.363	362.768	5.00E-05
S000005591	CYT1		778.333	1655.73	5.00E-05
S000001570	CYT2		54.4594	112.59	5.00E-05
S000001742	DAL80		8.16004	2.08592	5.00E-05
S000001908	DCV1		16.9573	7.6585	5.00E-05
S000000945	DDI1		74.8197	175.283	5.00E-05
S000001537	DEF1		41.6456	108.598	5.00E-05
S000000011	DEP1		38.1086	96.2962	5.00E-05
S000002819	DFM1		79.2034	171.101	5.00E-05
S000002182	DIA3		8.56165	25.7433	5.00E-05
S000004340	DIC1		98.4532	39.7888	5.00E-05
S000002671	DIN7		14.1526	6.59183	5.00E-05
S000002333	DLD1		298.623	614.14	5.00E-05
S000000797	DLD3		124.124	23.9581	5.00E-05
S000001157	DMA1		34.9185	73.2754	5.00E-05
S000002681	DON1		53.0696	24.8324	5.00E-05
S000006379	DPB2		10.6712	4.12135	5.00E-05
S000001779	DRE2		94.5168	211.308	5.00E-05
S000000926	DSE1		61.9612	235.333	5.00E-05
S000001186	DSE2		74.179	280.152	5.00E-05
S000005790	DSE3		47.0314	161.96	5.00E-05
S000005447	DUF1		25.5424	51.4517	5.00E-05

S000003029	DUO1		27.2991	11.825	5.00E-05
S000001762	DYN1		7.49561	18.9743	5.00E-05
S000003378	ECL1		338.629	145.893	5.00E-05
S000002854	ECM11		1.88702	0.901928	0.0088
S000000282	ECM33		533.41	258.715	5.00E-05
S000001923	ECO1		25.8328	9.30717	5.00E-05
S000006016	EEB1		19.4443	93.5092	5.00E-05
S000005271	EGT2		23.2748	71.0807	5.00E-05
S000005670	ELG1		11.5421	4.83643	5.00E-05
S000001531	ELM1		18.9646	8.56301	5.00E-05
S000000630	ELO2		34.7866	10.7484	5.00E-05
S000005518	ENB1		14.3896	30.0368	5.00E-05
S000003486	ENO1		6018.61	2213.83	5.00E-05
S000001217	ENO2		891.458	239.93	5.00E-05
S000004196	ENT2		57.6196	133.941	5.00E-05
S000004815	ERG2		54.4108	25.6872	5.00E-05
S000000671	ERS1		57.0074	27.8581	5.00E-05
S000005377	ESC8		14.5215	5.70535	5.00E-05
S000002773	ESF1		36.9496	125.478	5.00E-05
S000002203	FAD1		41.0761	87.5676	5.00E-05
S000001543	FBA1		8927.54	3708.04	0.00035
S000003691	FBP26		123.192	248.091	5.00E-05
S000000244	FIG1		3.62618	1.50175	0.00215
S000004334	FKS1		52.8209	20.2833	5.00E-05
S000006142	FLC1		74.5721	26.5141	5.00E-05
S000000049	FLC2		72.0173	33.2922	5.00E-05
S000001810	FLO10		4.40167	9.88842	5.00E-05
S000001458	FLO11		3.95506	11.021	5.00E-05
S000001360	FMC1		71.7881	149.38	5.00E-05
S000000984	FMP10		112.378	253.294	5.00E-05
S000002381	FMP45		344.401	162.079	5.00E-05
S000000026	FRT2		13.7638	28.0535	5.00E-05
S000005797	FSF1		29.8779	10.5813	5.00E-05
S000004835	FSH2		39.4558	79.1978	5.00E-05
S000000947	FTR1		67.1767	21.9971	5.00E-05
S000000017	FUN30		10.6042	5.07512	5.00E-05
S000000532	FUS1		5.41721	16.1563	5.00E-05
S000000563	FYV5		53.6393	22.6853	0.00015
S000004862	GAD1		506.923	1263.88	5.00E-05
S000004924	GAS1		236.377	92.0758	5.00E-05
S000004335	GAS2		6.31997	14.7144	5.00E-05
S000004828	GAS3		32.1934	14.9569	5.00E-05
S000005492	GAS4		9.31491	3.92491	5.00E-05
S000004003	GAT3		1.48607	0.227214	0.0091
S000002426	GCV1		51.5605	120.162	5.00E-05
S000005902	GDH1		176.968	34.4721	5.00E-05
S000000885	GET2		56.1867	116.358	5.00E-05
S000002766	GGA1		53.9787	118.199	5.00E-05
S000002717	GIC2		77.0967	29.5313	5.00E-05
S000000729	GIM4		70.9708	28.4045	5.00E-05
S000006239	GLN1		1413.56	347.361	5.00E-05
S000002916	GNP1		44.194	112.637	5.00E-05
S000005417	GPM3		5.11313	2.44273	0.0006
S000001315	GPP1		153.494	34.6016	5.00E-05
S000002925	GRH1		125.671	255.6	5.00E-05
S000004511	GSF2		118.438	249.121	5.00E-05
S000003149	GTS1		75.5311	169.671	5.00E-05
S000005763	HES1		4.58141	1.64637	5.00E-05
S000000857	HIS1		31.2286	68.1236	5.00E-05
S000005515	HPF1		153.376	395.333	5.00E-05
S000005483	HRP1		20.4443	49.4543	5.00E-05
S000004798	HSC82		302.73	881.908	5.00E-05
S000001584	HSL1		15.4426	7.59897	5.00E-05
S000005546	HSP10		1492.89	4077.74	5.00E-05
S000000276	HSP26		11941.7	28562	0.00165
S000004249	HSP60		289.298	1307.84	5.00E-05

S000005551	HST3		12.6187	29.0042	5.00E-05
S000003455	HSV2		43.0643	96.2453	5.00E-05
S000005262	HXT14		6.07631	0.711615	5.00E-05
S000000867	ICL1		4088.36	464.546	5.00E-05
S000006210	ICL2		100.718	47.043	5.00E-05
S000001913	IGD1		363.934	736.259	5.00E-05
S000000888	ILV1		40.0115	17.9469	5.00E-05
S000003777	ILV3		105.287	46.8998	5.00E-05
S000004773	INP2		12.0318	5.35861	5.00E-05
S000006130	IPL1		6.67534	2.52885	5.00E-05
S000000344	IRA1		23.0054	68.2492	5.00E-05
S000001288	IRR1		24.8777	8.01911	5.00E-05
S000006345	KAR3		13.2171	6.13242	5.00E-05
S000000529	KCC4		7.72001	3.16068	5.00E-05
S000001651	KKQ8		28.6411	62.5922	5.00E-05
S000005266	KRE1		244.557	514.844	5.00E-05
S000006363	KRE6		58.1755	28.598	5.00E-05
S000000564	KRR1		50.7126	24.4154	5.00E-05
S000002444	KRS1		86.4417	41.6851	5.00E-05
S000001593	KTI12		21.5891	50.4737	5.00E-05
S000004990	LAP2		47.8647	112.874	5.00E-05
S000000539	LSB5		124.319	249.809	5.00E-05
S000005925	LSP1		376.148	1349.78	5.00E-05
S000006478	LSR1		172.741	77.9434	5.00E-05
S000000022	LTE1		3.95674	1.65594	5.00E-05
S000002642	LYS4		33.4551	14.985	5.00E-05
S000001512	MAE1		70.395	13.1389	5.00E-05
S000000502	MAL31		47.9071	137.137	5.00E-05
S000000908	MAM1		5.94061	0.896602	5.00E-05
S000004153	MAS1		39.1518	85.8932	5.00E-05
S000002161	MCD1		15.1815	2.73712	5.00E-05
S000001648	MCD4		10.9932	4.87345	5.00E-05
S000000119	MCM2		12.2634	5.17899	5.00E-05
S000004264	MCM5		21.3624	8.75427	5.00E-05
S000003785	MDE1		87.283	35.5335	5.00E-05
S000005117	MDG1		149.376	383.984	5.00E-05
S000005486	MDH2		955.59	101.075	5.00E-05
S000005436	MDM20		5.57534	2.61294	5.00E-05
S000001237	MDM31		33.3365	80.7273	5.00E-05
S000005086	MEP2		57.4033	14.1865	5.00E-05
S000005425	MET22		36.7599	16.6617	5.00E-05
S000003578	MHP1		43.2283	89.1365	0.0002
S000002704	MHR1		110.214	232.68	5.00E-05
S000001572	MIF2		8.10317	3.01531	5.00E-05
S000001057	MIP6		11.325	4.00063	5.00E-05
S000002438	MIX14		248.983	502.197	5.00E-05
S000001313	MMF1		849.668	1774.27	5.00E-05
S000000745	MMS21		31.3593	13.0559	5.00E-05
S000004789	MMT1		10.7244	3.97495	5.00E-05
S000006145	MMT2		48.9674	107.75	5.00E-05
S000003556	MPS3		36.0947	9.83007	5.00E-05
S000000566	MRC1		14.4906	6.41787	5.00E-05
S000002755	MRP1		78.5918	189.208	5.00E-05
S000006039	MRP51		79.062	201.023	5.00E-05
S000002523	MRPL1		66.3446	137.482	5.00E-05
S000005228	MRPL10		63.9883	137.52	5.00E-05
S000004304	MRPL15		60.7655	123.713	5.00E-05
S000004806	MRPL24		79.261	158.961	5.00E-05
S000001621	MRPL31		110.65	240.609	5.00E-05
S000000455	MRPS5		57.7363	116.64	5.00E-05
S000004767	MRPS8		81.3599	166.324	5.00E-05
S000001760	MRS4		45.6506	106.351	5.00E-05
S000005962	MRX11		8.18346	3.2746	5.00E-05
S000004209	MSC3		49.8468	99.904	5.00E-05
S000006251	MSF1		15.6462	41.6091	5.00E-05
S000001891	MSH4		7.80467	3.73819	5.00E-05

S000002504	MSH6		17.0877	6.12822	5.00E-05
S000005017	MSK1		31.4699	81.0569	5.00E-05
S000005476	MSN1		29.2572	61.3684	5.00E-05
S000004193	MSS51		55.992	175.08	5.00E-05
S000003255	MTL1		62.3978	126.593	5.00E-05
S000005007	MTQ1		37.3963	82.5769	5.00E-05
S000000032	MTW1		13.23	6.27591	0.00015
S000002901	MZM1		79.5093	169.953	5.00E-05
S000005081	NAM9		37.6099	82.8409	5.00E-05
S000001269	NAS2		100.023	209.089	5.00E-05
S000029704	NBL1		48.9632	119.075	5.00E-05
S000003652	NCA3		242.931	89.2864	5.00E-05
S000002243	NDE2		403.539	149.432	5.00E-05
S000001811	NFT1		2.63752	6.15034	0.0001
S000005022	NIS1		26.7298	122.016	5.00E-05
S000005964	NOP4		26.4051	12.608	5.00E-05
S000002840	NPL3		236.104	486.225	5.00E-05
S000000270	NRG2		40.9794	18.4831	5.00E-05
S000003391	NSR1		72.171	23.6678	5.00E-05
S000000205	NTH2		35.5869	118.3	5.00E-05
S000002352	NUS1		34.5157	70.4512	5.00E-05
S000001238	NVJ1		93.5271	195.351	5.00E-05
S000002587	NVJ3		12.9325	6.29451	5.00E-05
S000001603	OAC1		15.5488	6.88094	5.00E-05
S000001021	OCA5		20.1834	7.17383	5.00E-05
S000004525	OGG1		10.8849	2.71174	5.00E-05
S000002177	OSH2		23.599	56.8348	5.00E-05
S000006117	OXR1		146.54	374.714	5.00E-05
S000004775	PAH1		33.6581	76.4117	5.00E-05
S000000775	PAU2		51.2551	23.9794	5.00E-05
S000000505	PAU24		6.22046	1.56915	0.00365
S000001805	PCK1		13006.1	5247.66	0.003
S000001312	PCL7		97.2576	274.102	5.00E-05
S000003319	PDC6		56.9142	14.8123	5.00E-05
S000004681	PDS5		17.7413	5.1877	5.00E-05
S000001919	PES4		12.0366	3.92118	5.00E-05
S000002486	PET100		227.102	475.64	5.00E-05
S000000860	PET117		38.2046	79.5364	5.00E-05
S000005328	PET494		60.8397	123.922	5.00E-05
S000005158	PEX17		28.133	56.8081	5.00E-05
S000003746	PEX2		65.3036	159.743	5.00E-05
S000005041	PHO23		65.4541	146.91	5.00E-05
S000005361	PHO80		28.3384	60.3171	5.00E-05
S000000500	PHO89		532.35	122.632	5.00E-05
S000002991	PIB2		33.272	15.6557	5.00E-05
S000004526	PIF1		14.9502	5.08483	5.00E-05
S000001307	PIG2		105.089	269.262	5.00E-05
S000005957	PMA2		46.6873	12.774	5.00E-05
S000000805	PMI40		124.998	43.9823	5.00E-05
S000005026	PMS1		14.2602	5.1492	5.00E-05
S000002251	PMT5		29.0733	13.2267	5.00E-05
S000003005	PNC1		748.624	2196.78	5.00E-05
S000000131	POL12		15.1358	4.52056	5.00E-05
S000005206	POL2		19.8076	9.26756	5.00E-05
S000002260	POL3		18.4654	8.90019	5.00E-05
S000000292	POL30		56.816	7.59958	5.00E-05
S000000607	POL4		17.897	8.92132	5.00E-05
S000003946	POM33		108.704	275.704	5.00E-05
S000005335	POP2		21.0986	48.8455	5.00E-05
S000000114	POP8		65.5325	22.4049	5.00E-05
S000003173	POX1		39.7415	18.1275	5.00E-05
S000006100	PPQ1		133.566	57.4097	5.00E-05
S000004004	PPR1		8.04974	2.87678	5.00E-05
S000003538	PRE3		206.669	426.227	5.00E-05
S000001528	PRI2		45.9779	15.6715	5.00E-05
S000004510	PRM6		1.56999	0.726036	0.02145

S000002197	PRM7		12.3802	5.65234	5.00E-05
S000006072	PRP46		41.6411	91.0317	5.00E-05
S000002420	PSF1		36.1999	15.5443	5.00E-05
S000003608	PSF2		29.1526	12.2572	5.00E-05
S000004368	PSY3		23.8654	10.1576	5.00E-05
S000000329	PTC4		38.9837	86.7983	5.00E-05
S000004132	PUT1		266.964	81.0944	5.00E-05
S000006390	PZF1		10.4835	5.1679	5.00E-05
S000001596	RAD27		54.702	18.6872	5.00E-05
S000004637	RCH1		85.2975	38.8357	5.00E-05
S000003126	RCK1		0.907207	2.04925	0.00075
S000002410	RCR2		80.906	210.355	5.00E-05
S000005440	REX4		6.6817	2.57417	5.00E-05
S000003709	RFA3		354.01	140.583	5.00E-05
S000004794	RGM1		59.3987	137.247	5.00E-05
S000000479	RIF1		10.7293	4.20422	5.00E-05
S000006129	RKM1		23.1871	10.2741	5.00E-05
S000003563	RNR2		656.912	235.085	5.00E-05
S000001328	RNR3		12.929	5.8921	5.00E-05
S000006044	RNY1		70.0274	141.064	5.00E-05
S000003112	ROG1		6.21026	1.23453	5.00E-05
S000001802	RPL40B		551.861	272.443	5.00E-05
S000002972	RPN14		47.4349	104.788	5.00E-05
S000002178	RPN4		107.09	226.373	5.00E-05
S000005642	RPO31		15.7736	7.26064	5.00E-05
S000002855	RPS17B		356.018	172.965	5.00E-05
S000000876	RPS24A		601.659	288.758	5.00E-05
S000004254	RPS28B		573.14	168.789	5.00E-05
S000005785	RPT4		149.313	327.815	5.00E-05
S000004738	RRB1		44.359	22.1417	5.00E-05
S000005813	RRP36		14.1121	5.87274	5.00E-05
S000002448	RSM10		146.068	294.959	5.00E-05
S000000852	RSM18		180.458	403.379	5.00E-05
S000002582	RSM24		82.4541	169.395	5.00E-05
S000001355	RSM25		69.9233	150.577	5.00E-05
S000002902	RSM28		83.4667	173.785	5.00E-05
S000003874	RSM7		145.594	306.278	5.00E-05
S000003384	RSR1		26.4995	12.8263	5.00E-05
S000001197	RTT107		11.9577	4.30889	5.00E-05
S000003764	SAG1		30.899	117.69	5.00E-05
S000002589	SAS4		39.8908	19.5865	5.00E-05
S000001026	SBP1		307.344	660.55	5.00E-05
S000002588	SCC2		7.01125	2.09239	5.00E-05
S000000241	SCO1		54.9502	141.667	5.00E-05
S000003616	SCP160		19.7791	6.59806	5.00E-05
S000006491	SCR1		394.527	83.4736	5.00E-05
S000004921	SCW10		232.743	63.1808	5.00E-05
S000002996	SCW11		21.7642	46.8948	5.00E-05
S000003856	SFC1		1575.38	589.095	5.00E-05
S000004313	SFH1		102.943	288.829	5.00E-05
S000001751	SHB17		34.78	13.952	5.00E-05
S000001366	SHQ1		12.8214	5.72571	5.00E-05
S000004069	SIC1		121.756	269.615	5.00E-05
S000001385	SIM1		96.4103	47.7435	5.00E-05
S000003625	SIP4		49.4443	17.2082	5.00E-05
S000004177	SKG3		4.99724	1.75975	5.00E-05
S000001192	SKG6		11.3666	4.55236	5.00E-05
S000005602	SKI7		11.3225	5.28689	5.00E-05
S000005947	SKS1		116.101	53.9221	5.00E-05
S000005187	SLA2		28.1404	13.0372	5.00E-05
S000002210	SLC1		20.3888	47.1944	5.00E-05
S000005721	SLK19		21.3183	8.93237	5.00E-05
S000005948	SMA1		21.9702	10.6394	5.00E-05
S000001886	SMC1		12.4307	4.70995	5.00E-05
S000001927	SMC2		11.225	5.17955	5.00E-05
S000003610	SMC3		12.7769	3.99847	5.00E-05

S000004375	SMC6		15.141	6.37701	5.00E-05
S000004941	SNO4		17.2319	5.23923	5.00E-05
S000006508	snR128		471.242	173.22	0.0155
S000007314	snR189		34.5492	139.131	5.00E-05
S000006509	snR190		313.005	106.112	5.00E-05
S000006493	snR4		188.185	584.205	5.00E-05
S000007291	snR5		54.0563	164.175	5.00E-05
S000000752	SNU13		48.7726	105.013	5.00E-05
S000005317	SOL1		38.363	79.7005	5.00E-05
S000003944	SPA2		16.8166	7.01999	5.00E-05
S000001215	SPC97		6.54459	3.00919	5.00E-05
S000001196	SPO16		19.2941	3.66877	5.00E-05
S000004619	SPO20		6.08078	2.52626	5.00E-05
S000005451	SPO21		3.58188	1.69242	0.00055
S000000454	SPO23		7.68161	3.74351	5.00E-05
S000003138	SPO74		8.12777	2.18233	5.00E-05
S000005740	SPR2		7.02646	0.707545	5.00E-05
S000002626	SPR28		14.8589	4.39385	5.00E-05
S000002931	SPS1		7.77015	3.24914	5.00E-05
S000001181	SPS100		373.099	26.2331	5.00E-05
S000005148	SPS18		7.439	16.4087	5.00E-05
S000004791	SPT21		8.30861	3.18704	5.00E-05
S000000611	SRD1		9.65748	36.9941	5.00E-05
S000004707	SRT1		8.56668	4.07485	0.00025
S000001569	SRX1		61.2841	27.1613	5.00E-05
S000000004	SSA1		377.933	1475.85	5.00E-05
S000003806	SSC1		288.244	676.652	5.00E-05
S000005768	SSP2		6.11932	2.98996	0.00015
S000004444	SST2		8.01389	18.1046	5.00E-05
S000005738	STE4		39.7401	89.1623	5.00E-05
S000005553	STI1		224.694	715.193	5.00E-05
S000000514	STP22		33.0824	70.7547	5.00E-05
S000005010	SUN4		18.9679	49.2848	5.00E-05
S000000626	SYP1		26.8509	57.2351	5.00E-05
S000000774	TCA17		20.4779	10.1352	0.00035
S000000248	TCM62		25.003	53.2488	5.00E-05
S000004905	TDA1		10.2681	22.4309	5.00E-05
S000003769	TDH2		696.909	116.251	5.00E-05
S000005864	TEA1		11.6286	4.88116	5.00E-05
S000004168	TFS1		808.94	2264.44	5.00E-05
S000005276	THI12		13.1387	2.63089	5.00E-05
S000002403	THI13		15.115	5.43365	5.00E-05
S000000444	THI2		13.1317	3.24661	5.00E-05
S000003376	THI4		15.8403	6.00268	5.00E-05
S000001836	THI5		6.51072	1.24872	5.00E-05
S000006278	TKL1		51.4511	24.1726	5.00E-05
S000002268	TMA17		213.333	669.589	5.00E-05
S000002512	TMS1		37.1841	83.1501	5.00E-05
S000000977	TMT1		80.8443	172.747	5.00E-05
S000002865	TOM1		19.6768	53.2079	5.00E-05
S000005571	TOM6		462.569	988.817	5.00E-05
S000004173	TOS4		15.9511	4.97272	5.00E-05
S000005244	TOS6		267.011	56.2321	5.00E-05
S000006124	TPK2		179.383	380.303	5.00E-05
S000005023	TPM1		481.714	985.912	5.00E-05
S000003370	TPO2		12.0682	3.62106	5.00E-05
S000001141	TRA1		17.4149	44.3031	5.00E-05
S000005243	TRF5		5.62468	1.92388	5.00E-05
S000002654	TRS23		90.4018	214.354	5.00E-05
S000004202	TUB4		25.7709	11.7357	5.00E-05
S000002507	TVP15		171.659	371.4	5.00E-05
S000006270	UBA3		17.7546	37.7808	5.00E-05
S000002249	UBX3		68.3148	148.459	5.00E-05
S000003251	UGA1		117.21	329.322	5.00E-05
S000002369	UGA4		12.5853	5.58886	5.00E-05
S000003605	UTP18		14.7552	4.63911	5.00E-05

S000001239	UTP9		14.0369	6.67193	5.00E-05
S000000764	UTR4		67.0155	169.799	5.00E-05
S000000309	VID24		48.9836	259.145	5.00E-05
S000003072	VPS73		22.9927	52.2468	5.00E-05
S000003193	VRG4		34.3022	13.2708	5.00E-05
S000004080	XDJ1		30.8266	85.4673	5.00E-05
S000003141	XRN1		38.7073	80.3703	5.00E-05
S000000035	YAL037W		14.0299	6.79206	5.00E-05
S000001204	YAP1801		77.2045	157.554	5.00E-05
S000000067	YAR009C		2.21448	6.89914	5.00E-05
S000000080	YAT1		887.755	228.435	5.00E-05
S000000220	YBR016W		216.767	472.809	5.00E-05
S000028736	YBR056W-A		223.251	63.9115	5.00E-05
S000028600	YBR126W-A		816.743	1679.98	5.00E-05
S000000343	YBR139W		143.563	319.054	5.00E-05
S000000388	YBR184W		3.14447	1.48337	0.00075
S000028535	YBR200W-A		82.3783	30.9359	0.0083
S000087085	YBR201C-A		1493.8	590.087	5.00E-05
S000002733	YCG1		6.44187	2.97291	5.00E-05
S000000554	YCL049C		34.7716	141.214	5.00E-05
S000000597	YCP4		292.912	647.947	5.00E-05
S000028818	YCR024C-B		664.712	250.373	5.00E-05
S000006008	YDC1		229.285	474.205	5.00E-05
S000007588	YDL085C-A		144.854	52.9683	5.00E-05
S000002272	YDL114W		4.30079	1.88913	0.00035
S000002370	YDL211C		4.67391	1.57554	5.00E-05
S000002425	YDR018C		40.6452	85.4797	5.00E-05
S000002449	YDR042C		9.42851	3.73311	5.00E-05
S000028542	YDR246W-A		8.4726	22.4672	0.0267
S000002657	YDR249C		12.1478	5.57912	5.00E-05
S000007650	YDR381C-A		229.463	463.282	5.00E-05
S000000881	YER079W		290.852	714.008	5.00E-05
S000000960	YER158C		154.057	44.7762	5.00E-05
S000001903	YFH7		18.2594	43.7546	5.00E-05
S000001882	YFL012W		7.51743	3.40276	0.0033
S000028635	YGL188C-A		0	15.8833	0.00145
S000003253	YGR021W		48.5815	127.04	5.00E-05
S000007406	YGR027W-B		1.05665	2.58236	5.00E-05
S000003362	YGR130C		99.287	231.416	5.00E-05
S000003385	YGR153W		31.7408	14.6004	5.00E-05
S000003433	YGR201C		453.185	988.983	5.00E-05
S000003498	YGR266W		31.5018	80.0511	5.00E-05
S000001000	YHL008C		25.8754	59.4871	5.00E-05
S000028654	YHR214C-E		18.3523	8.4573	0.00405
S000001339	YIL077C		139.089	333.577	5.00E-05
S000001431	YIL169C		65.9912	177.512	5.00E-05
S000003789	YJR028W		1.10505	3.79497	5.00E-05
S000003791	YJR030C		24.3788	7.52818	5.00E-05
S000003876	YJR115W		76.0995	267.65	5.00E-05
S000003915	YJR154W		16.0942	5.21531	5.00E-05
S000001285	YKE4		72.2596	148.778	5.00E-05
S000001527	YKL044W		8.42499	20.6552	0.0005
S000001533	YKL050C		16.0512	5.66337	5.00E-05
S000001749	YKR041W		9.80446	4.66793	0.0001
S000004043	YLR053C		86.3677	32.5503	5.00E-05
S000004098	YLR108C		5.17712	18.4568	5.00E-05
S000004115	YLR125W		15.696	38.4052	5.00E-05
S000004116	YLR126C		45.6878	22.2267	5.00E-05
S000004139	YLR149C		103.392	223.482	5.00E-05
S000028525	YLR307C-A		9690.79	174.863	5.00E-05
S000004407	YLR415C		2.36733	5.19263	0.02385
S000000308	YMC2		8.65814	3.02622	5.00E-05
S000028688	YML100W-A		0	8.55634	0.02395
S000004649	YMR046C		6.6425	14.5271	0.00145
S000028693	YMR182W-A		0	2772.18	0.02395
S000004819	YMR206W		147.766	338.366	5.00E-05

S000004823	YMR210W		31.469	78.6775	5.00E-05
S000004858	YMR244W		8.3061	1.67143	5.00E-05
S000004865	YMR252C		27.2218	65.3382	5.00E-05
S000004940	YMR321C		20.3175	6.95876	5.00E-05
S000005078	YNL134C		441.01	1030.59	5.00E-05
S000005088	YNL144C		39.6691	123.006	5.00E-05
S000005346	YNR063W		9.90487	4.42453	5.00E-05
S000005349	YNR066C		12.2574	5.95637	5.00E-05
S000005545	YOR019W		41.4445	98.2711	5.00E-05
S000028587	YOR381W-A		0	10.334	0.02395
S000005912	YOR385W		111.669	44.9712	5.00E-05
S000004489	YOX1		52.8603	16.6879	5.00E-05
S000000387	YPC1		49.4734	113.768	5.00E-05
S000006321	YPR117W		14.7644	31.5805	5.00E-05
S000007362	YPR158C-D		6.56524	15.462	5.00E-05
S000006406	YPR202W		12.5098	2.63361	5.00E-05
S000005995	YTA6		28.8854	61.9717	5.00E-05
S000005185	ZWF1		149.515	548.381	5.00E-05

Table 4-A2. FPKM values of the differentially expressed genes in the S7 strain.

Gene	Gene short name	1 h			4 h		
		Blank	Exposed	P value	Blank	Exposed	P value
S000000355	APD1	187.853	565.393	5.00E-05	255.624	1216.56	5.00E-05
S000003456	AZR1	9.16318	38.756	5.00E-05	7.19018	63.2672	5.00E-05
S000004338	CIS1	37.1927	469.24	5.00E-05	123.551	1630.4	5.00E-05
S000178119	IRT1	16.0131	33.1446	5.00E-05	5.27051	49.8132	5.00E-05
S000006056	ISU1	152.576	554.446	5.00E-05	657.239	3096.27	5.00E-05
S000000908	MAM1	0.379797	1.08709	2.82E-02			
S000006092	OYE3	2.7255	6.0554	1.00E-04			
S000004453	PAU4	9.44933	4.35795	7.35E-03			
S000004610	PLB1	242.277	743.135	5.00E-05	126.114	519.71	5.00E-05
S000003429	SNG1	24.0678	436.399	5.00E-05	38.1372	1673.12	5.00E-05
S000002418	SNQ2	34.4115	369.734	5.00E-05	32.8696	1678.75	5.00E-05
S000006505	snR45	65.4916	30.9265	2.61E-02			
S000006494	snR6	233.784	0	1.35E-03			
S000028425	SPO24	467.482	1431.7	5.00E-05			
S000028535	YBR200W-A	6.20308	0	1.35E-03			
S000007393	YDR210W-B	3.25331	8.03696	5.00E-05			
S000003267	YGR035C	8.28935	65.6414	5.00E-05	3.42878	68.9311	5.00E-05
S000007408	YGR038C-B	0.482773	1.1999	1.75E-03			
S000028640	YGR204C-A	0	318.992	2.40E-02	0	281.851	0.02395
S000003979	YLL056C	24.6194	63.093	5.00E-05	24.5265	140.827	5.00E-05
S000004036	YLR046C	32.7099	443.99	5.00E-05	29.1247	467.309	5.00E-05
S000007377	YLR256W-A	1.15653	4.59166	5.00E-05	0.65172	3.01147	5.00E-05
S000004708	YMR102C	28.1886	65.9566	5.00E-05	5.5598	24.0268	5.00E-05
S000028712	YOR161C-C	0	17.582	8.15E-03			
S000006009	YPL088W	59.9321	142.601	5.00E-05			
S000003430	YPP1	49.6096	103.071	5.00E-05	42.4597	147.578	5.00E-05
S000005085	AAH1				51.0601	8.13053	5.00E-05
S000004121	ACE2				10.4197	27.6789	5.00E-05
S000000111	ACH1				1798.88	333.239	5.00E-05
S000004295	ACO1				1275.45	630.673	0.0025
S000000050	ACS1				122.529	41.9095	5.00E-05
S000004143	ACS2				226.121	454.441	5.00E-05
S000028518	ADF1				32.7671	5.52166	0.0012
S000005446	ADH1				3288.93	7742.7	0.00025
S000004918	ADH2				38.2467	6.60232	5.00E-05
S000000603	ADY2				129.014	14.7532	5.00E-05
S000001864	AGX1				636.608	204.32	5.00E-05
S000004099	AHP1				1665.27	4025.27	5.00E-05
S000004552	AIM33				164.558	45.5056	5.00E-05
S000001341	AIR1				19.1487	5.85794	5.00E-05
S000003658	ALB1				57.5494	9.44474	5.00E-05
S000005982	ALD6				883.475	2407.37	5.00E-05
S000005313	ALG12				25.4989	60.6408	5.00E-05
S000002989	ALK1				22.1035	50.1153	5.00E-05
S000003457	AMA1				2.49945	7.33055	5.00E-05
S000001586	APE1				166.67	400.862	5.00E-05
S000005009	AQR1				71.0525	13.1158	5.00E-05
S000000838	ARB1				242.538	118.656	5.00E-05
S000003624	ARG3				12.6438	3.6508	5.00E-05
S000003125	ARI1				12.2502	34.2919	5.00E-05
S000002788	ARO10				126.135	31.9116	5.00E-05
S000002508	ARX1				40.6888	5.42779	5.00E-05
S000001535	ASK1				37.9736	124.181	5.00E-05
S000002592	ATC1				41.4409	14.5933	5.00E-05
S000003721	ATG36				132.445	65.4518	5.00E-05
S000005285	ATO2				261.707	114.132	5.00E-05
S000004286	ATP14				2038.98	985.025	5.00E-05
S000006192	ATP15				2154.2	964.137	5.00E-05
S000007247	ATP18				2630.63	1208.76	5.00E-05
S000006224	ATP20				845.502	385.777	5.00E-05
S000005999	ATP4				1137.32	562.429	5.00E-05
S000000272	BAP2				244.723	88.2959	5.00E-05

S000003909	BAT2		791.034	281.921	5.00E-05
S000001082	BCD1		32.5085	13.4334	5.00E-05
S000001735	BCH2		11.2343	24.2848	5.00E-05
S000002769	BCP1		41.1167	17.7545	5.00E-05
S000004391	BDF1		34.8404	85.5573	5.00E-05
S000002707	BFR2		35.4636	2.70232	5.00E-05
S000001358	BMT5		16.22	3.69068	5.00E-05
S000004053	BMT6		17.922	5.41225	5.00E-05
S000003596	BNA3		21.1614	64.6575	5.00E-05
S000004257	BOP2		242.265	50.3031	5.00E-05
S000000193	BRN1		3.31414	7.56121	5.00E-05
S000005437	BRX1		60.5805	9.06299	5.00E-05
S000002195	BSC1		101.917	3.8854	5.00E-05
S000004064	BUD20		301.795	73.0011	5.00E-05
S000004616	BUD22		32.6161	12.8338	5.00E-05
S000000643	BUD23		52.6483	19.037	5.00E-05
S000003852	BUD4		11.8893	26.5021	5.00E-05
S000004216	BUR2		52.1188	23.8671	5.00E-05
S000006032	CAR1		233.046	898.945	5.00E-05
S000004430	CAR2		121.549	316.39	5.00E-05
S000004506	CAT2		230.65	76.1036	5.00E-05
S000004165	CBF5		138.99	48.6404	5.00E-05
S000000036	CDC19		820.865	1867.43	0.0003
S000003084	CDC20		19.7307	44.5865	5.00E-05
S000003730	CDC6		2.57328	7.7137	5.00E-05
S000002997	CGR1		53.3453	15.7301	5.00E-05
S000000569	CHA1		2219.8	614.009	5.00E-05
S000000242	CHS2		17.8441	78.9741	5.00E-05
S000001094	CIC1		65.1854	13.4907	5.00E-05
S000004811	CIK1		7.30422	15.6132	5.00E-05
S000005554	CIN5		4.56387	9.6896	0.0001
S000005284	CIT1		1802.04	820.58	0.0003
S000000598	CIT2		1216.64	266.09	5.00E-05
S000006205	CIT3		80.0272	27.0228	5.00E-05
S000003340	CLB1		16.5848	45.8228	5.00E-05
S000006323	CLB2		8.09541	31.6662	5.00E-05
S000000359	CNS1		35.6352	16.1117	5.00E-05
S000002304	COP1		43.0809	87.1909	5.00E-05
S000005324	COQ2		48.7881	103.903	5.00E-05
S000004028	COX12		2912.59	1335.11	5.00E-05
S000004997	COX5A		2559.7	1152.15	5.00E-05
S000004869	COX7		5296.62	2273.62	5.00E-05
S000004387	COX8		2268.68	1082.02	5.00E-05
S000002225	COX9		1884.35	821.11	5.00E-05
S000005829	CPA1		75.5916	29.747	5.00E-05
S000005626	CRC1		148.263	47.2332	5.00E-05
S000005557	CRS5		951.271	342.805	5.00E-05
S000000365	CSH1		18.6352	44.5932	5.00E-05
S000006121	CSM4		27.5719	13.1834	0.00025
S000002664	CTA1		197.511	66.7011	5.00E-05
S000000010	CYS3		68.7881	171.967	5.00E-05
S000004581	DAT1		35.3443	17.0255	5.00E-05
S000003324	DBF2		32.3556	66.6771	5.00E-05
S000002189	DBP10		24.4282	9.1754	5.00E-05
S000005056	DBP2		106.185	5.82918	5.00E-05
S000003046	DBP3		58.7198	10.4482	5.00E-05
S000001732	DBP7		12.5068	4.71848	5.00E-05
S000001212	DBP8		24.5849	11.7224	5.00E-05
S000004266	DBP9		38.6036	11.4823	5.00E-05
S000004784	DDR48		331.35	692.175	5.00E-05
S000028579	DGR1		0	12.9643	0.00145
S000001561	DHR2		5.43899	1.21058	5.00E-05
S000004429	DIF1		42.8085	95.388	5.00E-05
S000006187	DIM1		50.507	18.0897	5.00E-05
S000004119	DIP2		16.7119	5.36998	5.00E-05
S000003931	DRS1		32.3774	5.24799	5.00E-05

S000005350	DSE4		17.2785	34.7067	5.00E-05
S000000796	DSF1		152.243	339.706	5.00E-05
S000001449	DSN1		13.5813	29.1135	5.00E-05
S000000412	DUR1%2C2		22.0401	51.9218	5.00E-05
S000004545	DUS1		23.7405	10.418	5.00E-05
S000004393	DUS3		27.3657	11.0864	5.00E-05
S000001655	EBP2		84.9599	20.2392	5.00E-05
S000000139	ECM1		31.8891	12.6614	5.00E-05
S000000055	ECM13		225.296	109.466	5.00E-05
S000004735	ECM16		13.1724	3.74011	5.00E-05
S000001022	ECM29		12.2382	27.8347	5.00E-05
S000006016	EEB1		41.6824	84.369	5.00E-05
S000007608	EFG1		39.0751	12.0772	5.00E-05
S000001326	EFM4		75.649	27.1819	5.00E-05
S000004969	EFM6		4.35649	2.0758	0.0035
S000005271	EGT2		29.6193	104.355	5.00E-05
S000003732	ELO1		101.087	237.026	5.00E-05
S000001217	ENO2		1570.21	3434.15	0.0008
S000000451	ENP1		41.9221	12.8767	5.00E-05
S000003377	ENP2		18.1626	5.16466	5.00E-05
S000001165	EPT1		21.7807	60.4147	5.00E-05
S000004652	ERB1		23.7106	4.88414	5.00E-05
S000001049	ERG11		247.246	553.295	5.00E-05
S000004815	ERG2		229.631	538.125	5.00E-05
S000003292	ERG25		179.57	480.83	5.00E-05
S000004617	ERG5		88.4659	365.388	5.00E-05
S000004467	ERG6		83.0952	201.181	5.00E-05
S000002773	ESF1		31.9451	7.7269	5.00E-05
S000005337	ESF2		22.3934	8.21427	5.00E-05
S000001281	FAF1		22.0692	6.09837	5.00E-05
S000002428	FAL1		13.953	2.88618	5.00E-05
S000004369	FBP1		1202.81	15.748	5.00E-05
S000004041	FCF2		95.5886	38.9545	5.00E-05
S000000858	FCY2		340.63	54.4583	5.00E-05
S000002942	FIT1		1.60974	3.24169	0.00055
S000001393	FKH1		10.6456	24.6554	5.00E-05
S000000251	FMP23		79.1193	33.0577	5.00E-05
S000001717	FOX2		68.3513	33.9116	5.00E-05
S000005512	FRE7		109.336	42.723	5.00E-05
S000000138	FUI1		122.778	48.2906	5.00E-05
S000006183	FUM1		612.771	286.196	5.00E-05
S000000563	FYV5		67.7116	9.93218	5.00E-05
S000004058	FYV7		60.159	15.2268	5.00E-05
S000004071	GAL2		11.9267	23.9587	5.00E-05
S000001131	GAR1		131.986	62.2508	5.00E-05
S000004828	GAS3		25.8161	62.2287	5.00E-05
S000005006	GCD10		23.6106	8.18477	5.00E-05
S000002374	GDH2		277.683	113.755	5.00E-05
S000000058	GDH3		104.54	33.1472	5.00E-05
S000000541	GFD2		27.7995	3.35683	5.00E-05
S000000856	GIP2		70.4841	157.645	5.00E-05
S000006058	GIP3		20.0723	80.6575	5.00E-05
S000001226	GND1		142.429	469.488	5.00E-05
S000005218	GOR1		199.492	436.273	5.00E-05
S000002180	GPD1		246.856	726.544	5.00E-05
S000006364	GPH1		402.162	989.873	5.00E-05
S000004863	GTO3		31.322	66.6775	5.00E-05
S000000743	GTT3		36.5381	74.3257	5.00E-05
S000004830	GUA1		177.617	29.9621	5.00E-05
S000004903	HAS1		44.6257	8.5841	5.00E-05
S000007548	HBN1		27.2464	68.4248	5.00E-05
S000003570	HCA4		19.4041	2.94181	5.00E-05
S000004959	HEF3		46.9591	22.1687	5.00E-05
S000000128	HEK2		44.8621	90.0183	5.00E-05
S000004540	HMG1		178.656	385.863	5.00E-05
S000000238	HMT1		159.768	21.7482	5.00E-05

S000004635	HOF1		10.5649	28.7022	5.00E-05
S000006037	HOS3		20.7792	57.3481	5.00E-05
S000004292	HRI1		51.6704	120.075	5.00E-05
S000000615	HSP30		2860.6	1201.63	5.00E-05
S000005551	HST3		22.5177	52.1588	5.00E-05
S000003797	HUL4		5.48808	12.7659	5.00E-05
S000001949	HXK1		5571.65	13748.9	0.0017
S000005516	HXT11		8.09592	20.7286	5.00E-05
S000001433	HXT12		19.1804	41.8186	0.00015
S000001432	HXT12		6.97547	18.1888	5.00E-05
S000000795	HXT13		31.5234	156.963	5.00E-05
S000001134	HXT4		123.487	380.518	5.00E-05
S000001138	HXT5		395.607	147.723	5.00E-05
S000002750	HXT7		207.224	510.124	5.00E-05
S000003755	HXT9		5.96	12.3982	5.00E-05
S000000867	ICL1		526.451	30.6143	5.00E-05
S000004164	IDP2		467.425	20.8834	5.00E-05
S000004213	IFH1		22.6799	10.5451	5.00E-05
S000003519	IMA1		11.9723	41.6355	5.00E-05
S000005517	IMA2		20.7178	108.211	5.00E-05
S000003752	IMA5		2.41496	11.8247	5.00E-05
S000001259	IMD2		97.3671	196.171	5.00E-05
S000004520	IMD4		50.0341	18.9434	5.00E-05
S000001191	IMP3		39.3358	7.91212	5.00E-05
S000005019	IMP4		48.8929	12.6673	5.00E-05
S000001127	IPI1		19.4263	7.04529	5.00E-05
S000005126	IPI3		29.2162	7.08816	5.00E-05
S000006130	IPL1		3.67137	8.08285	5.00E-05
S000003587	IRC8		11.8798	27.8711	5.00E-05
S000005752	ISU2		21.7697	44.18	5.00E-05
S000002900	IZH1		125.835	45.8492	5.00E-05
S000004013	IZH3		228.016	90.227	5.00E-05
S000005461	IZH4		13.2872	5.62201	5.00E-05
S000001700	JEN1		1798.63	449.406	5.00E-05
S000000912	KAP123		19.3605	7.74479	5.00E-05
S000000159	KIP1		5.57106	12.086	5.00E-05
S000002207	KNH1		48.0334	19.4755	5.00E-05
S000005076	KRE33		10.4862	3.45403	5.00E-05
S000005252	KRI1		86.4223	27.7336	5.00E-05
S000000564	KRR1		40.5852	10.3495	5.00E-05
S000002444	KRS1		247.373	95.8786	5.00E-05
S000007587	KTI11		132.934	53.4268	5.00E-05
S000005707	LAS17		34.5616	69.409	5.00E-05
S000000929	LCP5		39.3189	10.89	5.00E-05
S000003831	LIA1		90.6124	38.7315	5.00E-05
S000001626	LTV1		32.8989	4.5836	5.00E-05
S000002341	LYS20		98.9972	41.2656	5.00E-05
S000000023	MAK16		53.6908	10.152	5.00E-05
S000002467	MAK21		35.8686	5.66308	5.00E-05
S000000614	MAK31		75.2193	33.3689	5.00E-05
S000000346	MAK5		32.9674	8.74179	5.00E-05
S000001576	MBR1		221.566	108.732	5.00E-05
S000005833	MCH5		37.6744	13.5888	5.00E-05
S000006250	MCM16		8.83168	18.3764	0.00015
S000005486	MDH2		46.5847	97.4668	5.00E-05
S000004096	MDN1		10.7676	5.01117	5.00E-05
S000006342	MEP3		42.6308	87.405	5.00E-05
S000005154	MER1		11.1565	3.5999	5.00E-05
S000004294	MET17		161.968	547.054	5.00E-05
S000001456	MET28		13.2698	26.8952	0.00015
S000000893	MET6		101.991	242.282	5.00E-05
S000007547	MIC10		1479.55	670.75	5.00E-05
S000003838	MIR1		1136.52	441.678	5.00E-05
S000005061	MLS1		627.845	6.30485	5.00E-05
S000000145	MOH1		382.512	153.506	5.00E-05
S000003762	MPP10		42.8098	20.2024	5.00E-05

S000006316	MRD1		21.4885	3.06553	5.00E-05
S000002440	MRH1		438.923	888.66	5.00E-05
S000001492	MRT4		120.992	35.0583	5.00E-05
S000003586	MTR4		19.9305	4.90025	5.00E-05
S000001065	MYO1		5.6457	13.5065	5.00E-05
S000004715	MYO5		19.3341	49.3661	5.00E-05
S000005068	NAF1		58.0911	23.0234	5.00E-05
S000006047	NAN1		41.6908	7.21231	5.00E-05
S000005063	NCS2		31.4498	9.93515	5.00E-05
S000005464	NDJ1		31.6138	82.0301	5.00E-05
S000006147	NEW1		52.5829	16.0324	5.00E-05
S000002367	NHP2		180.049	87.2345	5.00E-05
S000006132	NIP7		64.8322	11.7825	5.00E-05
S000001213	NMD3		80.9893	14.3109	5.00E-05
S000005582	NOB1		56.9681	25.02	5.00E-05
S000005732	NOC2		40.3396	7.99347	5.00E-05
S000003992	NOC3		20.0016	8.94535	5.00E-05
S000006348	NOC4		40.515	10.5975	5.00E-05
S000006014	NOG1		72.0572	8.64138	5.00E-05
S000005336	NOG2		78.9496	6.05812	5.00E-05
S000002172	NOP1		181.998	45.3229	5.00E-05
S000005401	NOP12		37.3265	14.3978	5.00E-05
S000005119	NOP13		34.4373	8.92755	5.00E-05
S000002307	NOP14		22.7735	5.88889	5.00E-05
S000005054	NOP15		94.1589	15.6847	5.00E-05
S000000804	NOP16		126.313	53.5919	5.00E-05
S000003483	NOP19		35.4323	15.4137	5.00E-05
S000005005	NOP2		54.8526	9.7202	5.00E-05
S000005964	NOP4		27.7503	6.57465	5.00E-05
S000006067	NOP53		65.7385	24.1025	5.00E-05
S000004187	NOP56		106.524	31.0816	5.00E-05
S000005837	NOP58		113.971	29.1802	5.00E-05
S000002372	NOP6		86.3094	30.0695	5.00E-05
S000003335	NOP7		45.291	7.69183	5.00E-05
S000005504	NOP8		16.3309	4.76641	5.00E-05
S000003275	NQM1		466.848	187.437	5.00E-05
S000002326	NRP1		22.6096	5.25487	5.00E-05
S000000928	NSA2		68.5338	7.32972	5.00E-05
S000003391	NSR1		291.638	6.64972	5.00E-05
S000003744	NUC1		43.0242	19.0568	5.00E-05
S000000808	NUG1		51.2874	9.55769	5.00E-05
S000006055	ODC1		294.717	96.0916	5.00E-05
S000003023	OLE1		699.299	249.638	5.00E-05
S000001711	OSH6		20.1665	53.6194	5.00E-05
S000002896	PAC11		4.66999	10.2777	5.00E-05
S000001038	PAU13		0.886287	3.46419	0.0244
S000000437	PBP2		11.6945	26.6885	5.00E-05
S000001805	PCK1		1646.94	20.7071	5.00E-05
S000004034	PDC1		1335.65	3826.31	5.00E-05
S000005887	PDE2		140.368	37.855	5.00E-05
S000006206	PDH1		223.638	30.8802	5.00E-05
S000000548	PDI1		324.922	766.663	5.00E-05
S000003471	PEX21		81.47	31.5354	5.00E-05
S000000400	PGI1		331.225	677.723	0.00025
S000000605	PGK1		3812.07	9613.06	0.00035
S000001610	PGM1		22.3103	47.8136	5.00E-05
S000004711	PGM2		420.027	1328.45	5.00E-05
S000001526	PHD1		41.9611	89.4044	5.00E-05
S000002689	PHM6		11.6295	2.765	0.0016
S000000500	PHO89		484.324	160.984	5.00E-05
S000002782	PHO92		4.10004	1.69353	0.00065
S000001646	PIR3		46.5685	11.9775	5.00E-05
S000002976	PMA1		362.976	835.431	5.00E-05
S000005671	PNO1		112.916	30.9167	5.00E-05
S000005687	PNS1		66.8973	146.878	5.00E-05
S000003262	POP6		86.9081	39.8159	5.00E-05

S000001422	POT1		371.551	144.616	5.00E-05
S000005501	PPM2		6.37555	2.29944	5.00E-05
S000003355	PPT1		18.8305	8.54691	5.00E-05
S000006077	PRM4		84.425	28.6557	5.00E-05
S000002197	PRM7		18.8208	3.92585	5.00E-05
S000003088	PRP43		36.7307	7.73511	5.00E-05
S000001003	PRS3		121.64	45.0682	5.00E-05
S000000164	PRS4		80.2947	37.9673	5.00E-05
S000003820	PTK2		51.1523	107.094	5.00E-05
S000002904	PUF6		46.6409	6.72597	5.00E-05
S000000987	PUG1		16.2444	6.07847	5.00E-05
S000006133	PUS1		22.8864	7.17993	5.00E-05
S000004186	PWP1		44.2842	9.9437	5.00E-05
S000000653	PWP2		18.1727	3.91608	5.00E-05
S000003030	PYC1		418.981	149.106	5.00E-05
S000005627	RAS1		68.5006	27.6453	5.00E-05
S000005827	RAX1		20.0156	43.0105	5.00E-05
S000002935	RBA50		67.3365	27.7401	5.00E-05
S000000034	RBG1		47.6919	18.7907	5.00E-05
S000005370	RCL1		59.2294	14.3728	5.00E-05
S000000254	REG2		339.131	115.612	5.00E-05
S000000471	REI1		50.1351	12.1258	5.00E-05
S000005733	RET1		22.3691	10.6537	5.00E-05
S000001947	RET2		59.9478	123.245	5.00E-05
S000005440	REX4		19.0273	6.2546	5.00E-05
S000004063	RFU1		36.8525	11.0571	5.00E-05
S000001319	RGI2		923.288	250.236	5.00E-05
S000005633	RGS2		17.1454	3.78031	5.00E-05
S000001240	RIX1		16.2699	3.62487	5.00E-05
S000003957	RIX7		7.59802	2.43974	5.00E-05
S000005621	RKI1		152.191	6.10125	5.00E-05
S000003999	RLP24		123.542	30.0871	5.00E-05
S000004947	RLP7		88.1791	21.6735	5.00E-05
S000002873	RMT2		65.0987	7.13642	5.00E-05
S000003969	RNP1		9.9872	4.69256	0.0005
S000004852	RNT1		19.8475	5.16498	5.00E-05
S000003139	ROK1		24.6508	4.07377	5.00E-05
S000003824	RPA12		41.941	19.5013	5.00E-05
S000006214	RPA135		33.0288	8.67903	5.00E-05
S000005868	RPA190		19.5178	8.39026	5.00E-05
S000003684	RPA34		92.3185	23.2522	5.00E-05
S000005867	RPA43		16.8359	6.43367	5.00E-05
S000005192	RPA49		39.9354	8.21912	5.00E-05
S000005057	RPC19		89.9085	29.6924	5.00E-05
S000001733	RPC37		98.4236	32.9241	5.00E-05
S000006314	RPC40		87.3345	33.9684	5.00E-05
S000006394	RPC82		28.8919	14.4217	5.00E-05
S000001130	RPF1		55.2369	7.08492	5.00E-05
S000001789	RPF2		54.219	12.4802	5.00E-05
S000006490	RPR1		43.1246	3.68262	5.00E-05
S000004738	RRB1		72.6677	14.6744	5.00E-05
S000004507	RRN11		24.6288	2.75593	5.00E-05
S000002494	RRP1		31.3751	13.5626	5.00E-05
S000005933	RRP12		22.1193	4.23274	5.00E-05
S000001565	RRP14		91.5146	32.3794	5.00E-05
S000006347	RRP15		107.209	40.7015	5.00E-05
S000001107	RRP3		35.2231	12.0736	5.00E-05
S000005813	RRP36		14.8997	3.03933	5.00E-05
S000004842	RRP5		20.4435	4.92563	5.00E-05
S000002490	RRP8		38.2057	7.98598	5.00E-05
S000006341	RRP9		29.9531	13.3687	5.00E-05
S000005820	RRS1		70.8328	15.0523	5.00E-05
S000000641	RRT12		13.3876	31.204	5.00E-05
S000001389	RRT14		65.6931	18.7659	5.00E-05
S000003114	RRT6		72.0451	35.9495	5.00E-05
S000000668	RSA4		14.4283	2.48633	5.00E-05

S000005575	RSB1		28.6108	62.6128	5.00E-05
S000002910	SAM2		266.066	716.493	5.00E-05
S000003198	SAP4		11.0649	27.2637	5.00E-05
S000002312	SAS10		46.5983	10.9993	5.00E-05
S000000241	SCO1		184.589	385.878	5.00E-05
S000003511	SCW4		131.942	266.799	5.00E-05
S000003477	SDA1		24.727	5.48198	5.00E-05
S000003964	SDH2		2090.31	876.149	5.00E-05
S000000883	SER3		93.2234	31.9916	0.001
S000003704	SET2		15.3511	31.5162	5.00E-05
S000003856	SFC1		516.974	6.80135	5.00E-05
S000001534	SFK1		91.9825	251.633	5.00E-05
S000004328	SGD1		15.5357	7.61548	5.00E-05
S000000898	SHC1		29.7955	12.8495	5.00E-05
S000000127	SHE1		10.372	21.6455	5.00E-05
S000001366	SHQ1		14.0927	6.36135	5.00E-05
S000004787	SIP18		209.256	88.9344	5.00E-05
S000003625	SIP4		29.3473	7.26667	5.00E-05
S000000791	SIT1		31.6387	10.9142	5.00E-05
S000005947	SKS1		96.0132	28.0689	5.00E-05
S000003313	SLX9		36.0052	17.1323	5.00E-05
S000005854	SNC2		547.919	260.457	5.00E-05
S000007499	snR10		70.4846	28.5711	5.00E-05
S000007441	snR17b		6.56441	2.8189	0.00745
S000007295	snR19		38.3611	16.8673	5.00E-05
S000007497	snR30		46.4559	20.5841	5.00E-05
S000006500	snR34		52.8041	21.4327	0.00155
S000007299	snR35		91.206	19.8685	5.00E-05
S000006501	snR37		41.2445	14.6817	5.00E-05
S000006502	snR42		57.748	21.2125	5.00E-05
S000006497	snR8		32.0259	10.4309	0.0089
S000028467	snR82		66.6043	30.4606	0.00025
S000028466	snR84		13.6678	5.48542	0.00025
S000000752	SNU13		225.541	64.286	5.00E-05
S000005277	SNZ2		4.49376	2.10163	0.00125
S000003934	SOF1		36.0771	10.7185	5.00E-05
S000001206	SOL3		74.8867	234.992	5.00E-05
S000000559	SPB1		20.5588	3.90919	5.00E-05
S000002764	SPC110		5.70094	12.7206	5.00E-05
S000003468	SPG1		1405.53	299.512	5.00E-05
S000004713	SPG4		3067.38	176.87	5.00E-05
S000003291	SPR3		3.0491	6.70152	5.00E-05
S000001451	SQT1		64.5727	28.7824	5.00E-05
S000029010	SRG1		318.651	109.814	0.0001
S000005773	SRL1		211.119	472.955	5.00E-05
S000000542	SRO9		7.83162	1.64868	5.00E-05
S000001800	SRP40		48.832	19.1458	5.00E-05
S000000004	SSA1		1073.16	2530.2	5.00E-05
S000003947	SSA2		256.954	633.96	5.00E-05
S000000171	SSA3		337.378	64.4377	5.00E-05
S000000905	SSA4		1194.03	469.116	5.00E-05
S000002388	SSB1		240.388	102.351	5.00E-05
S000001108	SSF1		25.7443	2.87475	5.00E-05
S000002720	SSF2		33.5364	16.1095	5.00E-05
S000004795	SSO2		67.9522	145.554	5.00E-05
S000001424	SUC2		1156.3	2878.76	0.0001
S000005010	SUN4		57.0239	114.635	5.00E-05
S000004516	SUR7		109.322	299.943	5.00E-05
S000002553	SWI5		15.7371	50.4439	5.00E-05
S000004241	SYM1		109.592	239.721	5.00E-05
S000002221	SYO1		24.0398	4.35881	5.00E-05
S000000273	TAT1		52.01	8.16904	5.00E-05
S000005612	TCB1		38.8653	91.6447	5.00E-05
S000003437	TDA10		94.417	193.824	5.00E-05
S000003769	TDH2		733.766	1631.86	5.00E-05
S000003424	TDH3		9013.15	18936.3	0.00535

S000005864	TEA1		13.9746	5.55109	5.00E-05
S000006284	TEF1		502.197	219.567	5.00E-05
S000007255	TIM11		1296.84	621.529	5.00E-05
S000000271	TIP1		395.191	106.5	5.00E-05
S000000813	TIR1		8.13146	20.689	5.00E-05
S000005778	TMA16		75.293	33.6691	5.00E-05
S000004882	TMA23		45.3926	13.9745	5.00E-05
S000000150	TOD6		30.3814	7.89991	5.00E-05
S000003147	TOS3		4.52558	9.94242	5.00E-05
S000002457	TPI1		2773.56	5653.09	0.00115
S000005799	TPO4		31.6919	105.54	5.00E-05
S000002481	TPS2		367.746	841.396	5.00E-05
S000004874	TPS3		62.4782	149.064	5.00E-05
S000002527	TRM1		30.0375	11.2245	5.00E-05
S000005484	TRM11		20.6076	4.01879	5.00E-05
S000001764	TRM2		45.912	18.0282	5.00E-05
S000002572	TRM82		34.1831	11.2326	5.00E-05
S000004566	TSL1		251.263	756.358	5.00E-05
S000002218	TSR1		27.7624	10.9164	5.00E-05
S000006128	TYW1		66.9578	26.59	5.00E-05
S000005130	UBP10		63.249	26.1669	5.00E-05
S000001518	UGP1		435.749	1125.93	5.00E-05
S000000135	URA7		23.5139	3.99542	5.00E-05
S000001497	URB1		7.55547	2.8982	5.00E-05
S000003802	URB2		8.40794	3.45136	5.00E-05
S000005295	URK1		24.8087	9.82011	5.00E-05
S000004122	USB1		20.8489	43.4955	5.00E-05
S000003645	UTP10		20.4192	6.3316	5.00E-05
S000001582	UTP11		30.515	8.60303	5.00E-05
S000004212	UTP13		20.0604	2.91949	5.00E-05
S000004558	UTP14		26.2376	6.60511	5.00E-05
S000004699	UTP15		27.4197	8.57954	5.00E-05
S000003605	UTP18		20.1438	6.69323	5.00E-05
S000000100	UTP20		10.0083	4.53911	5.00E-05
S000004401	UTP21		16.3741	6.54742	5.00E-05
S000005530	UTP23		23.763	5.48938	5.00E-05
S000001353	UTP25		23.2735	4.70194	5.00E-05
S000002732	UTP4		26.1579	7.4968	5.00E-05
S000002806	UTP5		59.3851	10.1694	5.00E-05
S000002857	UTP6		17.7354	4.17601	5.00E-05
S000000884	UTP7		39.9913	15.6137	5.00E-05
S000003360	UTP8		19.7375	5.2625	5.00E-05
S000001239	UTP9		23.6829	8.6428	5.00E-05
S000001318	VHR1		46.2467	95.1409	5.00E-05
S000004329	VRP1		43.4327	90.0083	5.00E-05
S000005886	VTS1		18.2988	6.89055	5.00E-05
S000005227	WSC2		38.8785	81.6844	5.00E-05
S000001020	WSC4		6.78646	15.9827	5.00E-05
S000000080	YAT1		404.691	16.218	5.00E-05
S000000826	YAT2		287.437	23.8326	5.00E-05
S000000124	YBL028C		79.9966	25.5864	5.00E-05
S000000300	YBR096W		69.0069	149.934	5.00E-05
S000000388	YBR184W		1.82034	4.0215	0.00015
S000087085	YBR201C-A		205.331	66.3033	5.00E-05
S000000442	YBR238C		18.8461	3.21682	5.00E-05
S000000489	YBR285W		77.8389	158.592	5.00E-05
S000003435	YCH1		50.2899	109.711	5.00E-05
S000000658	YCR062W		22.1073	71.933	5.00E-05
S000007223	YCR087C-A		51.8858	19.3195	5.00E-05
S000000699	YCR102C		5.65637	2.39361	5.00E-05
S000007588	YDL085C-A		59.3175	122.057	0.0004
S000007234	YDR034W-B		117.987	39.6907	0.00575
S000002496	YDR089W		12.4409	27.742	5.00E-05
S000007410	YDR210W-D		1.28509	3.23265	0.0025
S000004239	YEF3		537.289	125.973	5.00E-05
S000007523	YER053C-A		5208.94	11439.2	0.0001

S000001828	YFL066C		2.46775	6.716	5.00E-05
S000003085	YGL117W		122.061	47.0811	5.00E-05
S000003211	YGL242C		37.7032	101.523	5.00E-05
S000003299	YGR067C		90.3979	12.4892	5.00E-05
S000003311	YGR079W		27.7187	6.40697	5.00E-05
S000003466	YHB1		29.6483	12.9533	5.00E-05
S000001253	YHR210C		6.16314	15.8296	5.00E-05
S000028654	YHR214C-E		27.6708	4.52051	5.00E-05
S000001262	YHR219W		1.04493	2.37515	0.0002
S000006122	YIG1		187.367	64.7199	5.00E-05
S000003754	YJL218W		22.7526	61.6029	5.00E-05
S000113563	YKL065W-A		78.9133	38.3711	0.0006
S000028524	YKL068W-A		91.8365	42.8701	0.0001
S000004098	YLR108C		22.8081	69.857	5.00E-05
S000004169	YLR179C		81.6098	284.051	5.00E-05
S000028808	YLR264C-A		0	143.359	0.02395
S000028525	YLR307C-A		13.3267	2.20411	0.01025
S000007620	YLR363W-A		62.8511	26.6302	5.00E-05
S000007380	YLR410W-B		1.43147	2.89034	0.0063
S000004454	YLR462W		1.01567	2.46662	0.0143
S000000308	YMC2		32.7712	10.4541	5.00E-05
S000004576	YML108W		122.451	48.0398	5.00E-05
S000004809	YMR196W		106.019	217.358	5.00E-05
S000004892	YMR279C		10.0013	22.0755	5.00E-05
S000004927	YMR310C		39.9385	17.3833	5.00E-05
S000004932	YMR315W		284.923	1123.2	5.00E-05
S000005003	YNL058C		68.2774	141.516	5.00E-05
S000005078	YNL134C		982.568	332.108	5.00E-05
S000007624	YNL162W-A		55.214	9.77154	5.00E-05
S000005356	YNR073C		71.8184	232.878	5.00E-05
S000005467	YOL107W		12.7124	27.2766	5.00E-05
S000005545	YOR019W		78.3074	37.9609	5.00E-05
S000003513	YOR1		20.2724	112.28	5.00E-05
S000005712	YOR186W		20.3651	9.59458	0.00035
S000005794	YOR268C		5.68748	2.80056	0.02625
S000005865	YOR338W		250.729	26.1151	5.00E-05
S000005914	YOR387C		13.4817	28.113	5.00E-05
S000122558	YPR010C-A		3780.66	1333.53	5.00E-05
S000113589	YPR145C-A		50.1257	15.9709	5.00E-05
S000004110	YPS1		51.1561	105.954	5.00E-05
S000005248	YPT11		11.6869	25.183	5.00E-05
S000002789	YRA1		133.042	286.643	5.00E-05
S000005798	YTM1		31.9286	6.27597	5.00E-05
S000005613	YVC1		29.2784	64.7019	5.00E-05
S000001465	YVH1		27.6367	10.2171	5.00E-05
S000003443	ZPR1		287.479	117.202	5.00E-05
S000003224	ZRT1		174.376	43.479	5.00E-05

Table 4-A3. FPKM values of the differentially expressed genes in the MS300c strain.

			1 h			4 h	
Gene	Gene short name	Blank	Exposed	P value	Blank	Exposed	P value
S000004708	ALD6	150.055	385.549	5.00E-05	194.561	1768.41	5.00E-05
S000003152	CHA1	196.027	454.089	3.00E-04	5053.3	1571.31	5.00E-05
S000005575	CIS1	36.392	317.822	5.00E-05	80.1899	4782.5	5.00E-05
S000005511	GND2	28.9101	63.3784	5.00E-05			
S000003979	GRE1	34.9014	78.5703	5.00E-05	117.954	386.145	5.00E-05
S000006509	GRE2	130.667	341.078	5.00E-05			
S000003430	HED1	3.43333	7.31453	4.00E-03			
S000000276	HSP26	806.57	2231.96	5.00E-05			
S000001456	IMA5	6.75864	22.7257	5.00E-05	7.94311	210.405	5.00E-05
S000007374	ISU1	792.979	1722.33	5.00E-05	4167.31	11906.6	5.00E-05
S000001319	MET17	123.808	323.091	5.00E-05	20.5788	82.6569	5.00E-05
S000004294	MET28	16.1913	33.1938	5.00E-05			
S000007225	OYE3	6.23214	12.55	5.00E-05	25.5585	368.598	5.00E-05
S000003513	PDH1	43.7223	91.1953	5.00E-05	1518.1	325.747	5.00E-05
S000002418	PDR16	100.574	290.518	5.00E-05	39.4016	406.872	5.00E-05
S000000569	PDR3	38.3887	85.148	5.00E-05	19.7875	114.54	5.00E-05
S000003267	PDR5	293.322	965.067	5.00E-05	95.9941	1899.66	5.00E-05
S000003752	RGI2	27.4341	55.2147	5.50E-04	4482.8	1065.54	5.00E-05
S000001318	RSB1	134.784	324.209	5.00E-05	152.98	680.187	5.00E-05
S000003429	SIP18	104.616	253.103	5.00E-05			
S000003488	SNG1	28.1045	407.768	5.00E-05	153.371	4338.36	5.00E-05
S000006009	SNQ2	63.6899	581.396	5.00E-05	95.3482	5364.8	5.00E-05
S000006092	snR190	73.7678	34.0164	2.40E-03	92.0523	41.226	1.55E-03
S000005982	STR3	27.7965	57.7412	5.00E-05			
S000006056	VHR1	49.2327	111.726	5.00E-05	178.506	439.246	5.00E-05
S000087203	YCL048W-A	38.3994	81.7119	5.50E-04	1285.51	464.376	5.00E-05
S000004338	YGR035C	51.5937	489.559	5.00E-05	26.0709	3179.55	5.00E-05
S000006206	YLL056C	10.7366	79.7965	5.00E-05	60.9014	6481.26	5.00E-05
S000005175	YLR035C-A	6.29303	2.08239	5.00E-05			
S000000101	YLR157C-B	2.61714	0.12082	5.00E-05			
S000005679	YLR256W-A	2.70615	15.5411	5.00E-05	3.62626	1.23907	5.00E-05
S000004787	YMR102C	26.3911	74.3493	5.00E-05	4.39458	80.7617	5.00E-05
S000113613	YOR1	25.756	54.4819	5.00E-05	96.0492	412.084	5.00E-05
S000007377	YPL088W	38.7958	84.2661	5.00E-05	60.5417	265.748	5.00E-05
S000006144	YPP1	38.6139	81.2831	5.00E-05	56.4095	356.328	5.00E-05
S000001838	AAD6				86.1165	36.4309	5.00E-05
S000001589	AAT1				6.88318	15.0587	5.00E-05
S000004902	ABZ2				33.2207	71.1691	5.00E-05
S000000111	ACH1				1444.83	372.594	5.00E-05
S000000050	ACS1				444.074	120.96	5.00E-05
S000005446	ADH1				799.996	2085.02	5.00E-05
S000002634	ADK1				90.8589	220.746	5.00E-05
S000002624	ADR1				565.823	236.993	5.00E-05
S000000603	ADY2				92.9207	11.9106	5.00E-05
S000003039	AFT1				20.5869	50.1604	5.00E-05
S000000336	AGP2				229.788	93.8669	5.00E-05
S000001013	AIM17				3707.41	592.043	5.00E-05
S000001420	AIM20				14.2327	6.45579	3.00E-04
S000006079	AIM44				86.047	42.2462	5.00E-05
S000004780	ALD2				239.83	116.315	5.00E-05
S000005901	ALD4				3891.67	1647.41	1.00E-04
S000000875	ALD5				85.5098	181.398	5.00E-05
S000005313	ALG12				10.04	20.4428	5.00E-05
S000001844	ALR2				63.1662	30.5904	5.00E-05
S000002518	ALT2				223.918	100.436	5.00E-05
S000003457	AMA1				32.6834	14.0912	5.00E-05
S000003808	ANB1				0.408621	3.76334	1.69E-02
S000000762	ANP1				14.8019	39.7767	5.00E-05
S000001168	ANS1				2.21394	0.621638	1.37E-02
S000000555	APA1				116.653	283.196	5.00E-05
S000002938	APA2				410.266	185.944	5.00E-05

S000000355	APD1		444.961	1029.5	5.00E-05
S000005021	APJ1		1270.48	345.862	5.00E-05
S000003493	APL6		4.30858	14.6	5.00E-05
S000006396	AQY1		510.433	178.095	5.00E-05
S000003073	ARC1		73.7479	154.62	5.00E-05
S000001496	ARC19		106.099	259.678	5.00E-05
S000003624	ARG3		28.4074	70.2085	5.00E-05
S000004645	ARG80		273.661	123.559	5.00E-05
S000003125	ARI1		13.1155	100.719	5.00E-05
S000005972	ARL3		20.2915	47.5075	5.00E-05
S000002788	ARO10		37.9602	12.5204	5.00E-05
S000003116	ARO2		33.7234	80.3466	5.00E-05
S000000453	ARO4		9.08174	24.8698	5.00E-05
S000001179	ARO9		90.7884	28.9352	5.00E-05
S000002513	ARP10		23.2694	5.37418	5.00E-05
S000002508	ARX1		5.01155	27.1161	5.00E-05
S000004722	ASC1		48.4341	136.646	5.00E-05
S000001535	ASK1		40.275	213.414	5.00E-05
S000002592	ATC1		30.7122	90.315	5.00E-05
S000000332	ATG14		123.254	50.6359	5.00E-05
S000005442	ATG19		411.033	188.589	5.00E-05
S000004179	ATG26		184.947	84.4324	5.00E-05
S000000174	ATG8		2723.45	1237.55	5.00E-05
S000006230	ATH1		178.146	71.1647	5.00E-05
S000005285	ATO2		1767.31	387.349	5.00E-05
S000003716	ATP12		39.6303	100.516	5.00E-05
S000005303	ATP23		11.8923	27.9953	5.00E-05
S000005605	ATX2		1.80575	8.78132	5.00E-05
S000000790	AVT2		16.8673	6.16743	5.00E-05
S000005045	AVT4		346.67	154.161	5.00E-05
S000003456	AZR1		11.7813	25.9832	5.00E-05
S000001251	BAT1		98.4631	527.769	5.00E-05
S000003909	BAT2		2736.59	959.473	5.00E-05
S000000056	BDH1		3715.24	1406.56	5.00E-05
S000002707	BFR2		4.71014	27.6849	5.00E-05
S000003518	BIO2		29.4372	13.5801	5.00E-05
S000006138	BMS1		15.9927	34.1131	5.00E-05
S000001358	BMT5		8.49439	22.4114	5.00E-05
S000005110	BNI5		7.09616	15.5732	5.00E-05
S000004257	BOP2		464.186	83.3934	5.00E-05
S000006261	BRR1		10.2501	27.3703	5.00E-05
S000002195	BSC1		12.3127	70.3772	5.00E-05
S000003374	BTN2		2823.84	1048.28	5.00E-05
S000005990	BTS1		5.48458	12.2466	5.00E-05
S000000755	BUD16		9.61636	27.4052	5.00E-05
S000005310	BUD17		8.84989	24.4007	5.00E-05
S000005604	BUD21		21.3836	64.5021	5.00E-05
S000004616	BUD22		8.86088	32.2717	5.00E-05
S000001871	BUD27		11.5284	33.6061	5.00E-05
S000004216	BUR2		19.2527	44.9669	5.00E-05
S000005249	BXI1		1924.21	933.743	2.50E-04
S000003509	CAB4		20.3147	54.4132	5.00E-05
S000005802	CAF20		34.2172	104.316	5.00E-05
S000004506	CAT2		1075.99	346.716	5.00E-05
S000004893	CAT8		257.593	80.6562	5.00E-05
S000003268	CAX4		15.6912	51.0257	5.00E-05
S000004165	CBF5		24.2076	108.474	5.00E-05
S000003449	CCH1		1.95569	4.53842	5.00E-05
S000003382	CCM1		14.4683	31.1074	5.00E-05
S000001774	CCP1		1352.81	606.729	5.00E-05
S000001404	CCT2		54.4196	119.511	5.00E-05
S000002596	CCT6		65.709	164.615	5.00E-05
S000003647	CCT7		21.6549	58.7494	5.00E-05
S000000335	CCZ1		1.1008	3.31491	5.00E-05
S000004299	CDA2		0.768676	3.13721	3.50E-04
S000004205	CDC123		11.7703	33.4755	5.00E-05

S000000036	CDC19		212.418	668.421	5.00E-05
S000005783	CDC31		784.892	342.695	5.00E-05
S000003730	CDC6		1.08879	2.23664	2.50E-03
S000006081	CDC60		14.142	88.4787	5.00E-05
S000000863	CEM1		372.899	163.087	5.00E-05
S000006149	CET1		14.2169	33.2231	5.00E-05
S000002997	CGR1		29.0457	90.757	5.00E-05
S000001094	CIC1		14.4274	58.5056	5.00E-05
S000003694	CIS3		26.9871	12.4198	5.00E-05
S000005284	CIT1		3621.52	1463.06	5.00E-05
S000000598	CIT2		5996.69	1854.52	5.00E-05
S000006205	CIT3		1930.82	186.371	5.00E-05
S000004200	CLB4		3.67008	7.72492	5.00E-05
S000003342	CLD1		354.59	164.084	5.00E-05
S000004812	CLN1		7.14243	3.0912	5.00E-05
S000000038	CLN3		41.9318	15.9513	5.00E-05
S000005776	CLP1		17.276	35.9927	5.00E-05
S000028514	CMC4		1692.71	709.541	5.00E-05
S000005376	CMK2		547.167	258.097	5.00E-05
S000002315	CMR1		1.3521	3.09368	3.00E-04
S000000359	CNS1		20.5445	50.8433	5.00E-05
S000028527	COA2		1705.79	748.472	5.00E-05
S000000932	COM2		13.5006	32.1235	5.00E-05
S000002304	COP1		12.9447	28.6974	5.00E-05
S000005324	COQ2		7.32758	20.2143	5.00E-05
S000000141	COR1		2042.1	979.783	1.50E-04
S000005358	COS10		20.2229	9.14321	5.00E-05
S000003159	COX13		8324.16	2925.5	5.00E-05
S000007245	COX19		328.409	152.871	5.00E-05
S000113555	COX26		4147.07	1129.71	5.00E-05
S000004869	COX7		8747.41	2705.82	5.00E-05
S000002225	COX9		3582.99	1479.41	5.00E-05
S000003793	CPR7		7.1364	25.732	5.00E-05
S000003708	CPS1		370.727	82.0663	5.00E-05
S000005626	CRC1		416.191	137.067	5.00E-05
S000001189	CRP1		680.481	231.068	5.00E-05
S000005557	CRS5		4736.99	2298.42	5.00E-05
S000006121	CSM4		100.826	11.2262	5.00E-05
S000002664	CTA1		1311.67	245.176	5.00E-05
S000004568	CUE4		203.772	71.9089	5.00E-05
S000002368	CWC2		5.10841	16.875	5.00E-05
S000001579	CWP1		23.4427	6.33568	5.00E-05
S000004518	CYB2		2790.11	861.68	5.00E-05
S000005055	CYB5		19.0741	45.17	5.00E-05
S000003809	CYC1		2763.96	1161.77	5.00E-05
S000000765	CYC7		2868.07	1418.7	5.00E-05
S000000010	CYS3		14.294	36.1966	5.00E-05
S000001468	DAL2		391.558	182.837	5.00E-05
S000003913	DAL5		94.4777	23.994	5.00E-05
S000001742	DAL80		79.8301	32.9826	5.00E-05
S000006091	DAP1		217.947	564.818	5.00E-05
S000003324	DBF2		107.855	47.5522	5.00E-05
S000002189	DBP10		8.81575	21.5137	5.00E-05
S000003046	DBP3		8.61819	40.7559	5.00E-05
S000005572	DBP5		18.5068	42.0928	5.00E-05
S000005321	DBP6		4.23428	14.3392	5.00E-05
S000001732	DBP7		3.59969	11.613	5.00E-05
S000001212	DBP8		8.49056	22.3284	5.00E-05
S000004266	DBP9		10.9149	27.7472	5.00E-05
S000001187	DCD1		1.33186	2.79279	6.35E-03
S000005706	DCI1		39.8144	17.7708	5.00E-05
S000005509	DCP1		19.499	46.7713	5.00E-05
S000001833	DDI2		4.95683	1.96319	1.20E-03
S000005279	DDI3		9.56341	4.74254	9.50E-04
S000001311	DFG10		88.7354	43.8269	5.00E-05
S000004935	DIA1		115.388	49.4964	5.00E-05

S000004119	DIP2		1.94961	13.0451	5.00E-05
S000002333	DLD1		1574.32	781.994	5.00E-04
S000001085	DOG2		186.325	88.3826	5.00E-05
S000004133	DPH6		2.90528	10.039	5.00E-05
S000003931	DRS1		6.41241	17.6225	5.00E-05
S000000024	DRS2		3.26892	8.89837	5.00E-05
S000004545	DUS1		9.30406	22.6791	5.00E-05
S000004397	DUS4		13.7171	34.6617	5.00E-05
S000001762	DYN1		36.1046	11.7926	5.00E-05
S000001110	DYS1		21.0548	68.5664	5.00E-05
S000000744	EAF5		15.6719	32.0807	5.00E-05
S000001655	EBP2		38.4545	135.665	5.00E-05
S000000055	ECM1		5.461	15.1601	5.00E-05
S000002854	ECM11		2.32758	0.918933	4.90E-03
S000000139	ECM13		156.403	349.575	5.00E-05
S000004735	ECM16		3.19183	8.93892	5.00E-05
S000007608	EFG1		13.8997	40.4566	5.00E-05
S000003233	EFM5		32.8801	75.42	5.00E-05
S000004969	EFM6		3.36273	1.4476	4.70E-03
S000004825	EFR3		6.44013	14.4031	5.00E-05
S000002793	EFT2		41.0194	91.6305	5.00E-05
S000001236	EGD2		163.834	350.582	5.00E-05
S000007525	EGO4		16733.3	6166.68	5.00E-05
S000000381	EHT1		521.085	244.564	5.00E-05
S000004633	EIS1		484.808	208.202	5.00E-05
S000003432	ELP2		8.71132	22.8663	5.00E-05
S000006007	ELP3		7.52779	28.9898	5.00E-05
S000006022	ELP4		19.6397	47.1512	5.00E-05
S000004176	EMG1		9.6219	21.9972	5.00E-05
S000005257	EMW1		2.19375	6.52027	5.00E-05
S000002447	ENA1		241.417	40.8369	5.00E-05
S000003486	ENO1		514.492	1997.94	5.00E-05
S000000451	ENP1		19.211	52.9296	5.00E-05
S000003377	ENP2		3.00112	11.1157	5.00E-05
S000004055	ENV10		97.3576	47.8193	5.00E-05
S000004652	ERB1		4.18412	16.5725	5.00E-05
S000002822	ERD1		8.40385	18.5838	5.00E-05
S000003407	ERG1		73.2035	173.907	5.00E-05
S000001049	ERG11		62.0465	229.63	5.00E-05
S000004617	ERG5		25.0101	53.2573	5.00E-05
S000005337	ESF2		6.13135	15.3827	5.00E-05
S000001804	ESL2		141.182	69.3914	5.00E-05
S000005577	ETT1		11.0655	76.5977	5.00E-05
S000005844	FAA1		3349.15	901.575	5.00E-05
S000000817	FAA2		146.626	58.4204	5.00E-05
S000002325	FAP7		20.1907	53.3082	5.00E-05
S000004228	FAR10		5.37578	18.0552	5.00E-05
S000001670	FAT3		67.6071	13.9467	5.00E-05
S000001543	FBA1		976.788	2689.82	5.00E-05
S000003691	FBP26		370.176	182.898	5.00E-05
S000004041	FCF2		54.5548	123.326	5.00E-05
S000005915	FDH1		8.28768	2.6589	5.00E-05
S000006196	FDH2		17.5751	3.40866	1.70E-03
S000006197	FDH2		44.5364	5.56521	5.00E-05
S000000305	FES1		4467.32	1517.75	5.00E-05
S000004662	FET3		96.4202	208.005	1.50E-04
S000000244	FIG1		2.97033	1.26509	4.30E-03
S000005909	FIT2		82.469	470.108	5.00E-05
S000005910	FIT3		579.569	271.237	5.00E-05
S000001458	FLO11		42.4588	18.6054	5.00E-05
S000001254	FLO5		65.0436	27.9723	5.00E-05
S000001396	FLX1		6.71361	14.4895	5.00E-05
S000002381	FMP45		901.497	257.475	5.00E-05
S000001757	FMP46		3030.36	1479.24	5.00E-05
S000005200	FOL1		12.059	29.0263	5.00E-05
S000001717	FOX2		337.024	124.118	5.00E-05

S000004539	FPR3		53.2534	134.178	5.00E-05
S000004441	FPR4		19.7407	62.5795	5.00E-05
S000005911	FRE5		242.37	98.2527	5.00E-05
S000006062	FRK1		36.9318	17.9171	5.00E-05
S000004050	FRS1		10.6238	30.661	5.00E-05
S000001872	FRS2		60.0994	123.776	5.00E-05
S000005851	FRT1		102.312	36.2629	5.00E-05
S000005797	FSF1		19.8437	87.452	5.00E-05
S000000947	FTR1		16.1064	72.6189	5.00E-05
S000002134	FUN19		821.549	302.498	5.00E-05
S000001170	FUR1		12.7829	31.3316	5.00E-05
S000000532	FUS1		29.5573	11.233	5.00E-05
S000004071	GAL2		20.0846	9.13566	5.00E-05
S000001747	GAP1		298.192	147.812	1.00E-04
S000004828	GAS3		21.4087	9.50049	5.00E-05
S000003163	GCN1		4.11763	9.96294	5.00E-05
S000002426	GCV1		1049.59	498.382	5.00E-05
S000004801	GCV2		158.518	78.7606	1.50E-04
S000006388	GDB1		636.334	216.436	5.00E-05
S000002374	GDH2		526.805	231.738	1.00E-04
S000000058	GDH3		2932.12	826.992	5.00E-05
S000004742	GID8		1123.09	383.799	5.00E-05
S000000249	GIP1		100.486	45.4491	5.00E-05
S000006058	GIP3		35.0815	212.312	5.00E-05
S000000695	GIT1		46.9184	8.10298	5.00E-05
S000000737	GLC3		515.531	135.88	5.00E-05
S000003673	GLG2		187.462	83.7837	5.00E-05
S000004463	GLO1		1802.25	863.193	1.50E-04
S000002330	GLT1		77.0321	37.1552	5.00E-05
S000004437	GMC2		11.1438	2.79251	5.00E-05
S000001877	GNA1		70.5172	32.1828	5.00E-05
S000001226	GND1		73.199	175.526	5.00E-05
S000000822	GPA2		695.124	300.365	5.00E-05
S000004894	GPI12		163.896	77.2908	5.00E-05
S000001635	GPM1		367.22	1284.25	5.00E-05
S000005417	GPM3		4.33029	12.2077	5.00E-05
S000004233	GPN3		6.60334	22.8827	5.00E-05
S000002168	GRX6		211.657	97.5263	5.00E-05
S000003264	GSC2		744.632	292.159	5.00E-05
S000003639	GSM1		111.766	51.8652	5.00E-05
S000001911	GSY1		411.77	91.9463	5.00E-05
S000004248	GSY2		819.728	366.674	5.00E-05
S000004863	GTO3		42.3179	17.2947	5.00E-05
S000004830	GUA1		26.7586	101.209	5.00E-05
S000001417	GUT2		2654.69	802.533	5.00E-05
S000003627	GWT1		37.4985	18.6788	5.00E-05
S000002393	GYP7		487.878	196.408	5.00E-05
S000003830	HAM1		6.99165	22.8941	5.00E-05
S000004903	HAS1		6.80314	18.4637	5.00E-05
S000001792	HBS1		18.4686	38.889	5.00E-05
S000002382	HBT1		368.425	145.498	5.00E-05
S000004959	HEF3		354.915	108.29	5.00E-05
S000005763	HES1		12.5493	4.87636	5.00E-05
S000004716	HFD1		1315.92	648.251	3.00E-04
S000006175	HFI1		4.3899	11.1591	5.00E-05
S000003419	HGH1		3.27221	17.4061	5.00E-05
S000004976	HHT2		3100.4	1462.89	5.00E-05
S000000857	HIS1		391.367	167.556	5.00E-05
S000000452	HIS7		5.61375	21.4357	5.00E-05
S000003816	HIT1		40.02	81.017	5.00E-05
S000003908	HMS2		157.269	58.3305	5.00E-05
S000000238	HMT1		22.708	59.7097	5.00E-05
S000004195	HMX1		1568.56	588.841	5.00E-05
S000002565	HOM2		104.989	241.675	5.00E-05
S000000854	HOM3		9.19947	39.9466	5.00E-05
S000004864	HOR7		28451.1	7855.12	5.00E-05

S000001372	HPM1		15.5773	31.9305	5.00E-05
S000004292	HRI1		13.9651	67.2847	5.00E-05
S000003949	HSP104		5049.1	1852.59	1.50E-04
S000000615	HSP30		18410.2	4356.78	5.00E-05
S000002578	HSP42		11953.5	3410.1	5.00E-05
S000006161	HSP82		10489.6	4990.71	8.35E-03
S000002599	HST4		4.10756	11.1256	5.00E-05
S000006439	HTL1		23.3207	53.6485	8.50E-04
S000001136	HXT1		8.30965	41.8996	5.00E-05
S000004613	HXT2		1793.98	878.801	5.50E-04
S000002753	HXT3		466.708	5495.26	5.00E-05
S000001134	HXT4		358.15	2492.4	5.00E-05
S000001138	HXT5		1635.12	536.158	5.00E-05
S000002750	HXT7		1081.55	482.615	5.00E-05
S000003750	HXT8		6.05795	35.3173	5.00E-05
S000003755	HXT9		4.73115	10.2651	5.00E-05
S000000867	ICL1		153.66	61.8475	5.00E-05
S000004089	ICT1		29.9942	78.7306	5.00E-05
S000004954	IDP3		211.971	48.8372	5.00E-05
S000004213	IFH1		15.2933	47.2318	5.00E-05
S000005383	IFM1		23.8687	67.486	5.00E-05
S000001913	IGD1		1757.91	794.354	5.00E-05
S000003593	IKS1		195.944	94.2387	5.00E-05
S000003777	ILV3		54.4447	279.358	5.00E-05
S000004347	ILV5		274.359	579.801	5.00E-05
S000005517	IMA2		17.019	54.3198	5.00E-05
S000001259	IMD2		49.0382	12.6846	5.00E-05
S000001191	IMP3		6.81779	23.7791	5.00E-05
S000005019	IMP4		39.8731	87.7639	5.00E-05
S000005635	INP53		8.59035	19.0156	5.00E-05
S000001127	IPI1		5.47889	13.7202	5.00E-05
S000005126	IPI3		7.08107	17.874	5.00E-05
S000005441	IRA2		382.747	134.468	5.00E-05
S000002948	IRC4		20.2824	8.30562	5.00E-05
S000001952	IRC7		11.3029	39.9344	5.00E-05
S000178119	IRT1		15.7713	163.837	5.00E-05
S000003950	ISA1		734.318	308.209	5.00E-05
S000004686	ISF1		5158.64	1167.98	5.00E-05
S000006310	ISR1		151.263	66.9269	5.00E-05
S000000449	ISW1		5.18363	13.7257	5.00E-05
S000005831	ISW2		15.7206	34.0187	5.00E-05
S000004013	IZH3		459.705	221.034	5.00E-05
S000005461	IZH4		21.2768	9.66193	5.00E-05
S000001700	JEN1		1148.83	212.989	5.00E-05
S000002883	JIP4		171.242	84.2084	5.00E-05
S000003698	JJJ2		5.07667	11.2057	5.00E-05
S000003858	JJJ3		11.572	24.5568	2.50E-04
S000003210	KAP114		3.45503	6.98434	5.00E-05
S000000912	KAP123		4.60181	16.4579	5.00E-05
S000003571	KAR2		1491.37	719.109	7.00E-04
S000001644	KDX1		34.2648	16.7594	5.00E-05
S000005266	KRE1		1374.72	637.495	1.50E-04
S000005076	KRE33		2.17766	5.19743	5.00E-05
S000000564	KRR1		9.41317	32.8538	5.00E-05
S000002444	KRS1		77.1692	195.44	5.00E-05
S000001771	LAS1		9.89278	29.2072	5.00E-05
S000005707	LAS17		16.1696	32.6866	5.00E-05
S000004911	LCB1		15.4674	31.8935	5.00E-05
S000005977	LCL1		185.347	88.4678	5.00E-05
S000000929	LCP5		6.7935	29.896	5.00E-05
S000000102	LDB7		173.488	362.858	5.00E-05
S000005407	LDS2		77.9495	27.1	5.00E-05
S000005975	LEE1		646.031	263.906	5.00E-05
S000005976	LGE1		487.645	232.657	5.00E-05
S000003831	LIA1		25.843	55.8578	5.00E-05
S000001897	LOC1		45.8584	92.5694	5.00E-05

S000001688	LOS1		7.10436	14.8577	5.00E-05
S000005291	LRO1		73.6799	35.0944	5.00E-05
S000003067	LSG1		6.31745	17.3148	5.00E-05
S000028521	LSO2		66.4605	147.508	5.00E-05
S000001473	LYS1		145.8	59.6615	5.00E-05
S000002341	LYS20		411.925	186.186	5.00E-05
S000001512	MAE1		32.7139	80.9351	5.00E-05
S000001504	MAK11		11.9932	31.1389	5.00E-05
S000000023	MAK16		6.30295	15.8463	5.00E-05
S000002467	MAK21		3.82417	11.3742	5.00E-05
S000003521	MAL11		270.524	122.554	5.00E-05
S000000502	MAL31		370.593	178.343	5.00E-05
S000001066	MAS2		69.7651	140.602	5.00E-05
S000001576	MBR1		1296.74	574.652	5.00E-05
S000005479	MCH4		382.686	172.578	5.00E-05
S000001412	MCM10		3.90955	10.6361	5.00E-05
S000003169	MCM6		4.51747	15.6012	5.00E-05
S000000406	MCM7		9.18707	20.2087	5.00E-05
S000005486	MDH2		1684.47	767.897	1.00E-04
S000005086	MEP2		1906.73	555.133	5.00E-05
S000003496	MES1		14.0374	57.2318	5.00E-05
S000001390	MET18		2.84314	5.83912	5.00E-05
S000001308	MET30		248.365	108.328	5.00E-05
S000003905	MGM101		25.2525	51.2544	5.00E-05
S000001678	MIA40		331.226	753.188	5.00E-05
S000007618	MIM2		387.488	111.053	5.00E-05
S000000288	MIS1		3.3633	7.9942	5.00E-05
S000001411	MLP2		5.41567	14.5861	5.00E-05
S000005061	MLS1		103.443	25.4115	5.00E-05
S000006368	MMS1		2.73629	7.04553	5.00E-05
S000003719	MNN11		11.0769	24.2819	5.00E-05
S000000145	MOH1		1812.23	879.17	5.00E-05
S000001205	MPC2		1829.48	887.128	5.00E-05
S000003475	MPC3		2144.16	608.537	5.00E-05
S000005703	MPC54		38.988	18.3261	5.00E-05
S000005814	MPD1		123.297	33.6269	5.00E-05
S000003921	MPH3		1.33626	0.457529	6.00E-04
S000002978	MPO1		82.5784	36.5615	5.00E-05
S000005307	MPP6		19.9128	45.2454	5.00E-05
S000006316	MRD1		5.34064	15.3692	5.00E-05
S000006322	MRI1		10.7112	25.7172	5.00E-05
S000005129	MRPL19		102.667	217.856	5.00E-05
S000004838	MRPL44		236.579	479.087	5.00E-05
S000005250	MRPS18		188.891	402.191	5.00E-05
S000001492	MRT4		83.7312	222.008	5.00E-05
S000003763	MRX12		5.68446	12.0841	5.00E-05
S000001162	MSH1		4.72128	10.9105	5.00E-05
S000002602	MSS116		39.4901	106.148	5.00E-05
S000001677	MST1		11.9663	33.6788	5.00E-05
S000006018	MSY1		22.0751	46.9827	5.00E-05
S000003255	MTL1		287.616	132.611	5.00E-05
S000001669	MTR2		531.885	193.841	5.00E-05
S000003390	MTR3		6.05754	14.0658	5.00E-05
S000003586	MTR4		4.65686	16.7437	5.00E-05
S000004585	NAB6		160.013	70.9061	5.00E-05
S000005068	NAF1		27.9689	56.4602	5.00E-05
S000004685	NAM7		21.7727	45.3812	5.00E-05
S000006047	NAN1		12.453	33.739	5.00E-05
S000000120	NCL1		2.87697	9.63118	5.00E-05
S000005063	NCS2		9.3975	22.7798	5.00E-05
S000006147	NEW1		8.41593	33.0256	5.00E-05
S000004587	NGL3		360.208	118.621	5.00E-05
S000004926	NIP1		9.35661	42.1027	5.00E-05
S000006132	NIP7		5.68082	21.8491	5.00E-05
S000005067	NMA111		9.39518	27.7159	5.00E-05
S000001213	NMD3		29.1449	62.002	5.00E-05

S000005732	NOC2		7.24038	39.5135	5.00E-05
S000003992	NOC3		5.42577	16.7165	5.00E-05
S000006348	NOC4		9.0344	19.0266	5.00E-05
S000006014	NOG1		16.5865	47.5555	5.00E-05
S000005336	NOG2		18.006	53.0487	5.00E-05
S000002172	NOP1		33.7775	94.0263	5.00E-05
S000005401	NOP12		8.74745	42.5469	5.00E-05
S000005119	NOP13		5.04947	17.2993	5.00E-05
S000002307	NOP14		4.3521	14.3584	5.00E-05
S000005054	NOP15		28.0703	87.0679	5.00E-05
S000003483	NOP19		15.5802	42.1382	5.00E-05
S000005005	NOP2		10.0212	36.8038	5.00E-05
S000005964	NOP4		9.54809	24.4932	5.00E-05
S000006067	NOP53		30.6447	71.355	5.00E-05
S000004187	NOP56		13.4245	37.706	5.00E-05
S000005837	NOP58		12.2108	60.5629	5.00E-05
S000002372	NOP6		39.6519	85.7853	5.00E-05
S000003335	NOP7		11.0811	24.5102	5.00E-05
S000003547	NOP9		6.92809	19.7845	5.00E-05
S000005195	NRD1		85.4983	34.7918	5.00E-05
S000002326	NRP1		4.27142	13.5698	5.00E-05
S000000928	NSA2		10.2453	41.1802	5.00E-05
S000001175	NSG1		8.68009	18.4025	5.00E-05
S000003391	NSR1		63.3732	160.093	5.00E-05
S000000205	NTH2		304.399	152.153	5.00E-05
S000003744	NUC1		5.82663	13.465	5.00E-05
S000000808	NUG1		12.6961	25.4146	5.00E-05
S000001540	NUP120		2.8545	9.94587	5.00E-05
S000003060	NUP145		9.35841	20.4187	5.00E-05
S000001603	OAC1		67.2475	370.651	5.00E-05
S000006055	ODC1		494.019	219.357	5.00E-05
S000005748	ODC2		117.993	38.9661	5.00E-05
S000001398	OM45		3877.51	1896.43	8.00E-04
S000006398	OPT2		374.662	61.3168	5.00E-05
S000000264	ORC2		7.70143	16.366	5.00E-05
S000004342	ORM2		1811.23	742.481	5.00E-05
S000004044	OSW2		19.4164	9.61808	5.00E-05
S000002946	PAD1		116.307	37.6586	5.00E-05
S000004775	PAH1		354.279	93.4179	5.00E-05
S000002659	PAM1		167.814	81.2155	5.00E-05
S000001105	PAN5		10.8259	29.2496	5.00E-05
S000000673	PAT1		42.5583	92.9046	5.00E-05
S000001805	PCK1		1736.79	398.985	5.00E-05
S000001113	PCL5		1341.41	531.936	5.00E-05
S000004034	PDC1		268.596	596.825	5.00E-05
S000003217	PDE1		452.96	187.513	5.00E-05
S000002814	PDR15		112.784	422.752	5.00E-05
S000005208	PDR17		17.9498	41.3107	5.00E-05
S000000860	PET117		81.0096	210.906	5.00E-05
S000003471	PEX21		49.515	110.116	5.00E-05
S000005496	PFK27		61.9719	196.165	5.00E-05
S000004594	PGA3		32.9019	185.822	5.00E-05
S000000605	PGK1		1742.98	4980.95	5.00E-05
S000002689	PHM6		19.3274	4.72242	5.00E-05
S000005444	PHM7		152.559	30.9843	5.00E-05
S000002889	PHO8		461.014	193.191	5.00E-05
S000000500	PHO89		1283.86	48.2716	5.00E-05
S000001307	PIG2		440.811	149.884	5.00E-05
S000004610	PLB1		219.573	718.035	5.00E-05
S000002976	PMA1		242.006	624.655	5.00E-05
S000002974	PMC1		302.586	118.245	5.00E-05
S000005687	PNS1		161.931	80.0164	5.00E-05
S000004534	POB3		24.351	52.8189	5.00E-05
S000000552	POF1		6.66325	24.2782	5.00E-05
S000005000	POR1		4099.5	1980.06	2.50E-04
S000001422	POT1		521.24	209.376	5.00E-05

S000003173	POX1		136.121	39.4148	5.00E-05
S000005501	PPM2		2.14591	7.3677	5.00E-05
S000004004	PPR1		3.00301	12.2814	5.00E-05
S000003355	PPT1		2.52324	5.85342	5.00E-05
S000001244	PPX1		31.2856	70.1655	5.00E-05
S000001357	PRK1		10.7146	22.2241	5.00E-05
S000006077	PRM4		103.01	46.3765	5.00E-05
S000002197	PRM7		12.3007	39.1428	5.00E-05
S000002708	PRO1		9.25751	21.3574	5.00E-05
S000003088	PRP43		3.72592	8.6486	5.00E-05
S000006072	PRP46		333.269	148.083	5.00E-05
S000002373	PRR2		200.368	79.7567	5.00E-05
S000001003	PRS3		50.8708	103.502	5.00E-05
S000005422	PRS5		29.2721	58.971	5.00E-05
S000005888	PRT1		22.2404	51.7804	5.00E-05
S000003608	PSF2		6.89973	16.3789	5.00E-05
S000005474	PTH4		37.1671	12.9526	5.00E-05
S000001801	PTR2		191.021	44.4983	5.00E-05
S000002904	PUF6		11.2264	54.3085	5.00E-05
S000004406	PUN1		175.291	59.8641	5.00E-05
S000006133	PUS1		3.51667	12.8771	5.00E-05
S000005236	PUS4		4.39158	14.5206	5.00E-05
S000005769	PUS7		6.076	18.6029	5.00E-05
S000004186	PWP1		6.08105	25.8284	5.00E-05
S000000653	PWP2		1.86255	10.5448	5.00E-05
S000001798	PXL1		22.4617	8.99315	5.00E-05
S000003030	PYC1		2475.11	1141.34	8.50E-04
S000000422	PYC2		467.041	203.705	1.00E-04
S000003529	QCR10		3533.7	1502.93	5.00E-05
S000003702	QCR8		6673.54	2233.02	5.00E-05
S000003415	QCR9		7289.67	3288.58	5.00E-05
S000002261	QRI1		8.95516	19.7915	5.00E-05
S000004022	RAD5		3.75866	8.46463	5.00E-05
S000005194	RAD50		7.1	14.6482	5.00E-05
S000005627	RAS1		7.24026	18.4692	5.00E-05
S000005042	RAS2		1299.63	559.113	5.00E-05
S000002610	RAV2		411.652	185.642	5.00E-05
S000004074	RAX2		10.9606	5.05692	5.00E-05
S000000034	RBG1		9.89255	29.5424	5.00E-05
S000003126	RCK1		12.323	37.7446	5.00E-05
S000005746	RCN2		1942.41	725.309	5.00E-05
S000000254	REG2		678.442	286.935	5.00E-05
S000000471	REI1		12.9212	50.8057	5.00E-05
S000005743	RFC1		5.70467	14.0686	5.00E-05
S000005454	RFC4		5.89958	19.7565	5.00E-05
S000004166	RFX1		33.3807	14.7928	5.00E-05
S000001847	RGD2		7.01256	18.8566	5.00E-05
S000004794	RGM1		412.117	121.787	5.00E-05
S000001521	RGT1		95.2116	37.3389	5.00E-05
S000005107	RIA1		6.64383	22.8357	5.00E-05
S000005427	RIB2		10.4673	21.8604	5.00E-05
S000004029	RIC1		4.16837	10.4399	5.00E-05
S000001861	RIM15		5.84699	12.342	5.00E-05
S000001240	RIX1		2.09664	6.53813	5.00E-05
S000003957	RIX7		1.44047	5.89589	5.00E-05
S000000234	RKM3		4.38312	13.3693	5.00E-05
S000002498	RLI1		3.76869	16.7628	5.00E-05
S000003999	RLP24		25.2653	84.5963	5.00E-05
S000004947	RLP7		56.6805	122.165	5.00E-05
S000002663	RMD5		290.676	139.886	5.00E-05
S000002873	RMT2		17.0803	37.5938	5.00E-05
S000004848	RNA1		27.813	60.1434	5.00E-05
S000003139	ROK1		5.903	12.1131	5.00E-05
S000003302	ROM1		124.423	49.8637	5.00E-05
S000006269	ROX1		118.383	319.657	5.00E-05
S000006214	RPA135		3.80404	16.6723	5.00E-05

S000005868	RPA190		3.9487	16.5445	5.00E-05
S000003684	RPA34		26.0163	103.136	5.00E-05
S000005867	RPA43		1.58633	4.35703	2.00E-04
S000005192	RPA49		4.04418	12.3143	5.00E-05
S000000358	RPB5		43.3156	123.195	5.00E-05
S000003038	RPB9		20.1882	50.9967	5.00E-05
S000002452	RPC11		21.5878	53.684	5.00E-05
S000003548	RPC17		2.61478	17.9983	5.00E-05
S000005057	RPC19		12.0729	55.8222	5.00E-05
S000005095	RPC31		9.02818	19.5914	5.00E-05
S000005286	RPC34		5.55002	16.0387	5.00E-05
S000006314	RPC40		27.3118	75.552	5.00E-05
S000001130	RPF1		15.4154	41.0299	5.00E-05
S000001789	RPF2		13.6782	44.3765	5.00E-05
S000000283	RPG1		19.933	50.1819	5.00E-05
S000001381	RPI1		28.2714	13.4374	5.00E-05
S000004065	RPL10		391.58	1018.71	5.00E-05
S000006306	RPL11A		46.2298	104.556	5.00E-05
S000003317	RPL11B		54.4473	184.758	5.00E-05
S000000780	RPL12A		58.1522	205.297	5.00E-05
S000002826	RPL12B		88.4363	266.431	5.00E-05
S000002240	RPL13A		40.7361	124.664	5.00E-05
S000004750	RPL13B		150.803	428.951	5.00E-05
S000001489	RPL14A		61.6588	223.353	5.00E-05
S000000993	RPL14B		257.53	545.026	5.00E-05
S000001395	RPL16A		72.2923	297.969	5.00E-05
S000005013	RPL16B		45.3072	160.773	5.00E-05
S000001663	RPL17A		59.8038	251.27	5.00E-05
S000003713	RPL17B		53.1942	156.089	5.00E-05
S000005480	RPL18A		90.4319	322.915	5.00E-05
S000002156	RPL19A		209.529	632.251	5.00E-05
S000000123	RPL19B		268.83	774.938	5.00E-05
S000003103	RPL1B		86.8903	222.4	5.00E-05
S000004855	RPL20A		78.9495	290.276	5.00E-05
S000005839	RPL20B		137.409	383.37	5.00E-05
S000000395	RPL21A		49.2241	258.267	5.00E-05
S000006000	RPL21B		74.901	281.196	5.00E-05
S000004051	RPL22A		42.3005	158.293	5.00E-05
S000006436	RPL22B		24.0785	72.8625	5.00E-05
S000000183	RPL23A		102.604	319.918	5.00E-05
S000000919	RPL23B		207.605	461.289	5.00E-05
S000002999	RPL24A		50.0254	259.06	5.00E-05
S000005487	RPL25		283.536	678.219	5.00E-05
S000004336	RPL26A		185.581	437.761	5.00E-05
S000003266	RPL26B		118.947	297.033	5.00E-05
S000001052	RPL27A		97.1128	279.157	5.00E-05
S000002879	RPL27B		64.6809	307.221	5.00E-05
S000003071	RPL28		330.895	730.228	5.00E-05
S000006437	RPL29		517.55	1117.15	5.00E-05
S000002104	RPL2A		37.4217	200.814	5.00E-05
S000001280	RPL2B		68.8658	260.363	5.00E-05
S000005589	RPL3		101.618	412.862	5.00E-05
S000002998	RPL30		211.347	469.658	5.00E-05
S000002233	RPL31A		149.495	569.628	5.00E-05
S000000188	RPL32		255.056	832.74	5.00E-05
S000006064	RPL33A		160.429	438.802	5.00E-05
S000005760	RPL33B		41.8464	422.973	5.00E-05
S000002135	RPL34A		125.671	270.643	5.00E-05
S000002350	RPL35A		126.947	329.737	5.00E-05
S000002295	RPL35B		117.526	260.507	5.00E-05
S000004807	RPL36A		129.62	519.815	5.00E-05
S000006438	RPL36B		211.777	568.802	5.00E-05
S000004175	RPL37A		109.242	470.479	5.00E-05
S000002908	RPL37B		382.864	929.646	5.00E-05
S000004317	RPL38		187.88	516.252	5.00E-05
S000003725	RPL39		670.201	1878.11	5.00E-05

S000001410	RPL40A		316.814	819.363	5.00E-05
S000001802	RPL40B		141.598	469.99	5.00E-05
S000002343	RPL41A		0	11828	1.45E-03
S000005106	RPL42A		136.026	724.541	5.00E-05
S000001183	RPL42B		218.622	656.765	5.00E-05
S000006247	RPL43A		286.301	871.918	5.00E-05
S000003855	RPL43B		97.521	292.301	5.00E-05
S000000235	RPL4A		35.3491	70.8664	5.00E-05
S000002419	RPL4B		24.8174	96.9996	5.00E-05
S000006052	RPL5		67.791	316.029	5.00E-05
S000004538	RPL6A		72.7018	243.309	5.00E-05
S000004440	RPL6B		21.9843	124.679	5.00E-05
S000006119	RPL7B		18.3837	56.5601	5.00E-05
S000001025	RPL8A		24.4738	286.605	5.00E-05
S000003968	RPL8B		54.8644	251.13	5.00E-05
S000002178	RPN4		1124.44	488.642	5.00E-05
S000004332	RPP0		77.2018	181.813	5.00E-05
S000001104	RPP1		8.55451	21.8889	5.00E-05
S000002239	RPP1A		117.156	341.159	5.00E-05
S000002288	RPP1B		80.991	277.224	5.00E-05
S000005399	RPP2A		58.0381	194.042	5.00E-05
S000002790	RPP2B		98.5658	261.122	5.00E-05
S000006490	RPR1		49.9259	13.6945	5.00E-05
S000003446	RPS0A		55.1627	211.254	5.00E-05
S000004038	RPS0B		44.3932	239.298	5.00E-05
S000002432	RPS11A		90.576	508.001	5.00E-05
S000000252	RPS11B		80.5493	176.999	5.00E-05
S000005896	RPS12		146.509	430.822	5.00E-05
S000002471	RPS13		73.9367	278.818	5.00E-05
S000000627	RPS14A		439.284	946.944	5.00E-05
S000003727	RPS14B		62.176	373.132	5.00E-05
S000005400	RPS15		218.256	458.124	5.00E-05
S000002241	RPS16B		68.8094	241.998	5.00E-05
S000004486	RPS17A		164	475.617	5.00E-05
S000002855	RPS17B		54.629	204.741	5.00E-05
S000004488	RPS18B		63.9518	294.886	5.00E-05
S000005481	RPS19A		78.9182	246.713	5.00E-05
S000005246	RPS19B		115.121	315.6	5.00E-05
S000004433	RPS1A		71.3505	388.105	5.00E-05
S000004528	RPS1B		61.8619	397.918	5.00E-05
S000003091	RPS2		110.939	296.488	5.00E-05
S000001007	RPS20		146.415	467.744	5.00E-05
S000001765	RPS21A		83.5752	181.654	5.00E-05
S000003672	RPS21B		174.857	600.711	5.00E-05
S000003350	RPS23A		496.269	1119.67	5.00E-05
S000000876	RPS24A		114.336	516.828	5.00E-05
S000001331	RPS24B		67.8615	216.95	5.00E-05
S000003259	RPS25A		254.643	542.431	5.00E-05
S000003157	RPS26A		408.24	1056.17	5.00E-05
S000000933	RPS26B		40.9971	99.5283	5.00E-05
S000001063	RPS27B		231.482	815.649	5.00E-05
S000005693	RPS28A		350.07	828.622	5.00E-05
S000004254	RPS28B		62.2118	267.456	5.00E-05
S000002219	RPS29B		422.153	999.308	5.00E-05
S000005122	RPS3		212.469	544.106	5.00E-05
S000005708	RPS30B		1011.23	2390.03	5.00E-05
S000004157	RPS31		190.576	632.545	5.00E-05
S000003906	RPS4A		69.7978	290.619	5.00E-05
S000001246	RPS4B		75.3616	271.513	5.00E-05
S000003884	RPS5		105.191	595.575	5.00E-05
S000006011	RPS6A		62.6211	221.071	5.00E-05
S000000385	RPS6B		32.8137	154.375	5.00E-05
S000005622	RPS7A		65.8716	190.077	5.00E-05
S000005040	RPS7B		83.3983	194.226	5.00E-05
S000000168	RPS8A		59.5516	136.948	5.00E-05
S000000904	RPS8B		21.9961	90.4263	5.00E-05

S000006002	RPS9A		32.525	146.207	5.00E-05
S000000393	RPS9B		28.1958	171.347	5.00E-05
S000004738	RRB1		11.8213	46.1938	5.00E-05
S000001080	RRF1		54.9628	115.278	5.00E-05
S000005477	RRI2		65.7221	30.6999	5.00E-05
S000004507	RRN11		3.48897	10.7266	5.00E-05
S000001608	RRN3		73.4075	34.8324	5.00E-05
S000005933	RRP12		5.46673	22.5808	5.00E-05
S000001565	RRP14		49.8908	115.418	5.00E-05
S000006347	RRP15		44.0384	93.6971	5.00E-05
S000001107	RRP3		2.51032	10.0399	5.00E-05
S000005813	RRP36		2.34548	6.08622	5.00E-05
S000000631	RRP43		41.7878	124.043	5.00E-05
S000003327	RRP46		35.5905	77.8065	5.00E-05
S000004842	RRP5		4.10001	17.6015	5.00E-05
S000006341	RRP9		10.0105	27.5874	5.00E-05
S000002749	RRS1		12.0847	34.5412	5.00E-05
S000005820	RRS1		33.1152	77.1149	5.00E-05
S000001389	RRT14		17.9089	58.0088	5.00E-05
S000005408	RRT8		303.015	72.473	5.00E-05
S000000668	RSA4		1.39735	8.61782	5.00E-05
S000002711	RSC3		3.76257	7.52585	5.00E-05
S000004596	RSC9		6.94351	16.0071	5.00E-05
S000002448	RSM10		1174.22	489.111	5.00E-05
S000000351	RTC2		189.675	69.8962	5.00E-05
S000001129	RTC3		4988.96	1944.4	5.00E-05
S000006104	RTT10		3.15854	10.4753	5.00E-05
S000005742	RUD3		5.56609	16.8178	5.00E-05
S000002598	RVB1		26.9796	69.5043	5.00E-05
S000000484	SAF1		302.014	136.244	5.00E-05
S000003764	SAG1		245.775	107.164	5.00E-05
S000000845	SAH1		52.474	150.131	5.00E-05
S000004170	SAM1		19.4842	65.7421	5.00E-05
S000002910	SAM2		36.2891	79.2502	5.00E-05
S000006195	SAM3		233.566	75.8412	5.00E-05
S000003634	SAP185		11.342	23.6441	5.00E-05
S000002312	SAS10		14.3431	39.1908	5.00E-05
S000000241	SCO1		149.789	326.732	5.00E-05
S000003511	SCW4		108.939	38.2819	5.00E-05
S000003477	SDA1		12.0766	25.8078	5.00E-05
S000004012	SDO1		19.1231	46.6858	5.00E-05
S000000200	SEA4		3.92136	9.22066	5.00E-05
S000005309	SEC12		5.62617	14.4431	5.00E-05
S000005780	SEC63		6.39577	14.541	5.00E-05
S000002484	SED1		9989.28	3930.65	5.00E-05
S000002430	SES1		35.3953	74.9022	5.00E-05
S000003704	SET2		3.55765	13.9314	5.00E-05
S000004313	SFH1		9.61653	20.1126	5.00E-05
S000001534	SFK1		127.229	494.155	5.00E-05
S000004328	SGD1		12.1799	26.2213	5.00E-05
S000004802	SGS1		22.1581	10.8849	5.00E-05
S000001751	SHB17		12.1462	36.408	5.00E-05
S000000898	SHC1		61.1566	24.0885	5.00E-05
S000000127	SHE1		5.64225	2.71461	6.00E-04
S000004154	SHH4		141.872	41.5444	5.00E-05
S000001366	SHQ1		3.89612	11.6137	5.00E-05
S000004434	SIR3		4.9893	11.3471	5.00E-05
S000004977	SIW14		26.7659	56.9275	5.00E-05
S000006393	SKI3		4.09289	9.35401	5.00E-05
S000003181	SKI8		14.3904	30.429	5.00E-05
S000001367	SLM1		274.403	115.129	5.00E-05
S000003313	SLX9		17.6559	55.4896	5.00E-05
S000005834	SLY41		127.792	59.7276	5.00E-05
S000005140	SLZ1		132.355	38.9558	5.00E-05
S000001092	SMF2		148.99	61.6093	5.00E-05
S000007236	SNA2		731.561	343.495	5.00E-05

S000005854	SNC2		1787.05	884.626	5.00E-05
S000002353	SNF3		154.335	65.8711	5.00E-05
S000004701	SNO1		156.017	74.8702	5.00E-05
S000007499	snR10		174.441	65.3791	5.00E-05
S000007293	snR11		848.655	343.308	5.00E-05
S000006498	snR13		92.5378	0	2.29E-02
S000007441	snR17b		18.5111	5.69123	5.00E-05
S000007314	snR189		52.9873	21.5989	6.30E-03
S000007497	snR30		115.267	47.8508	5.00E-05
S000007297	snR32		61.5921	28.8084	6.85E-03
S000007299	snR35		189.626	49.8955	5.00E-05
S000007300	snR36		70.4897	15.5295	1.70E-03
S000006502	snR42		175.747	71.9242	5.00E-05
S000006503	snR43		161.087	31.1589	5.00E-05
S000006454	snR63		30.9923	14.8173	4.20E-03
S000028467	snR82		569.326	153.47	5.00E-05
S000028468	snR83		204.02	57.7842	5.00E-05
S000119075	snR86		212.038	88.5227	5.00E-05
S000006305	SNT309		720.994	324.745	5.00E-05
S000000752	SNU13		81.5403	374.658	5.00E-05
S000003573	SNX4		296.408	119.644	5.00E-05
S000004702	SNZ1		1219.73	353.894	5.00E-05
S000003934	SOF1		5.01455	20.2345	5.00E-05
S000000559	SPB1		2.94923	10.4109	5.00E-05
S000004056	SPC3		17.8906	42.323	5.00E-05
S000004136	SPE4		14.3179	29.2093	1.50E-04
S000003468	SPG1		11324.6	2416.33	5.00E-05
S000004713	SPG4		35376.2	10546.1	5.00E-05
S000004803	SPG5		1894.66	591.925	5.00E-05
S000000952	SPI1		41746.7	13713.1	5.00E-05
S000001178	SPL2		752.591	83.1526	5.00E-05
S000005740	SPR2		2.30683	0.440568	2.20E-02
S000005840	SPS4		8.07844	2.66995	5.00E-05
S000001451	SQT1		18.3692	51.2192	5.00E-05
S000002716	SRB7		36.5118	97.1071	5.00E-05
S000005773	SRL1		130.014	53.7231	5.00E-05
S000001799	SRL3		160.487	65.5412	5.00E-05
S000000542	SRO9		1.0327	4.53218	5.00E-05
S000001637	SRP102		4.76128	14.2505	5.00E-05
S000001800	SRP40		128.277	42.7027	5.00E-05
S000001701	SRY1		259.345	120.849	5.00E-05
S000000171	SSA3		4147.67	1443.72	5.00E-05
S000000905	SSA4		1478.96	483.886	5.00E-05
S000002388	SSB1		17.2316	70.954	5.00E-05
S000005153	SSB2		55.8908	272.95	5.00E-05
S000001108	SSF1		2.11718	6.93399	5.00E-05
S000006013	SSU1		976.151	324.394	5.00E-05
S000005573	STD1		14.716	53.2999	5.00E-05
S000005738	STE4		99.4841	36.7477	5.00E-05
S000001388	STH1		6.11517	15.1556	5.00E-05
S000002944	STL1		30.1971	14.883	5.00E-05
S000004140	STM1		83.618	277.627	5.00E-05
S000001424	SUC2		2645.18	1079.22	5.00E-05
S000006355	SUE1		2656.93	579.547	5.00E-05
S000000498	SUL1		26.9747	13.4453	5.00E-05
S000000347	SUP45		36.4608	97.0614	5.00E-05
S000004516	SUR7		106.133	35.6901	5.00E-05
S000005950	SUV3		11.7306	28.0589	5.00E-05
S000001224	SVP26		13.1798	37.9979	5.00E-05
S000000009	SWC3		4.04783	14.9141	5.00E-05
S000000379	SWD3		4.57099	2.06006	6.00E-04
S000005692	SWT1		20.7906	42.0053	5.00E-05
S000002803	SXM1		17.9703	41.306	5.00E-05
S000002824	SYF1		3.36703	13.3301	5.00E-05
S000002221	SYO1		7.83623	22.1881	5.00E-05
S000000465	TAE1		28.154	57.1487	5.00E-05

S000006252	TAH18		3.78049	11.4456	5.00E-05
S000003278	TAM41		332.482	127.57	5.00E-05
S000006049	TBF1		3.92274	10.671	5.00E-05
S000002620	TCP1		25.9063	71.2315	5.00E-05
S000003588	TDH1		586.244	1699.77	5.00E-05
S000000287	TEC1		431.557	159.535	5.00E-05
S000001797	TGL4		245.039	114.639	5.00E-05
S000005416	THI20		16.5421	33.716	5.00E-05
S000006249	THP3		112.313	52.3906	5.00E-05
S000001067	THR1		14.6555	37.133	5.00E-05
S000000649	THR4		41.9173	95.3545	5.00E-05
S000001767	TIF1		14.492	34.1408	5.00E-05
S000004873	TIF11		56.7872	135.319	5.00E-05
S000006367	TIF3		41.9738	130.884	5.00E-05
S000002837	TIF35		80.7759	187.326	5.00E-05
S000006245	TIF5		37.5132	78.1822	5.00E-05
S000000271	TIP1		3808.86	1270.69	5.00E-05
S000006244	TIP41		199.975	91.5071	5.00E-05
S000006278	TKL1		26.4141	100.769	5.00E-05
S000006657	TLC1		39.2617	18.3337	5.00E-05
S000004319	TMA10		44092.5	16220.3	5.00E-05
S000002957	TMA20		24.8581	60.0091	5.00E-05
S000005617	TMA46		23.0337	52.849	5.00E-05
S000003492	TNA1		455.961	204.554	5.00E-05
S000005366	TOP1		10.6485	24.2195	5.00E-05
S000000851	TPA1		10.3556	50.4843	5.00E-05
S000001141	TRA1		43.3847	20.4213	5.00E-05
S000005243	TRF5		5.01952	10.737	5.00E-05
S000003623	TRL1		1.40452	4.96602	5.00E-05
S000005951	TRM44		4.88597	22.4525	5.00E-05
S000000265	TRM7		7.85227	28.5427	5.00E-05
S000004476	TRM9		8.22978	19.2582	5.00E-05
S000000892	TRP2		12.7948	26.9454	5.00E-05
S000001694	TRP3		11.1293	31.6652	5.00E-05
S000002815	TRS120		2.56556	5.83651	5.00E-05
S000002515	TRS85		5.89584	15.7929	5.00E-05
S000002218	TSR1		8.99848	30.4049	5.00E-05
S000000370	TYR1		14.9118	35.347	5.00E-05
S000003417	TYS1		16.4293	36.9821	5.00E-05
S000001806	UBP11		144.123	70.1906	5.00E-05
S000003733	UBP12		6.70927	13.747	5.00E-05
S000000369	UBS1		145.729	66.9066	5.00E-05
S000004553	UFO1		10.9935	24.5199	5.00E-05
S000002369	UGA4		72.9769	30.9216	5.00E-05
S000001518	UGP1		413.794	196.926	5.00E-05
S000003666	URA2		1030.9	403.742	2.00E-04
S000003864	URA8		860.972	294.965	5.00E-05
S000001497	URB1		1.43809	4.55605	5.00E-05
S000003802	URB2		1.4588	4.28044	5.00E-05
S000006356	URN1		67.0269	28.4003	5.00E-05
S000006151	USV1		750.253	289.899	5.00E-05
S000003645	UTP10		4.17962	14.7941	5.00E-05
S000001582	UTP11		17.5471	35.9422	5.00E-05
S000004212	UTP13		1.29572	5.42547	5.00E-05
S000004558	UTP14		3.28218	16.7507	5.00E-05
S000004699	UTP15		5.41636	21.0368	5.00E-05
S000003605	UTP18		6.41881	18.2103	5.00E-05
S000000100	UTP20		4.23875	10.2908	5.00E-05
S000004401	UTP21		2.34327	5.91505	5.00E-05
S000003322	UTP22		5.27872	14.9371	5.00E-05
S000001353	UTP25		7.68505	21.0394	5.00E-05
S000002732	UTP4		3.14976	12.4126	5.00E-05
S000002857	UTP6		4.32471	14.1228	5.00E-05
S000003360	UTP8		2.59049	6.41697	5.00E-05
S000001239	UTP9		7.22154	18.8053	5.00E-05
S000003326	VAS1		29.687	61.0286	5.00E-05

S000004694	VBA1		282.848	92.6894	5.00E-05
S000002286	VCX1		443.187	215.528	5.00E-05
S000003252	VMA7		83.2165	179.093	5.00E-05
S000000777	VMA8		67.5909	157.467	5.00E-05
S000004563	VPS9		11.1848	26.5546	5.00E-05
S000005457	WRS1		14.6282	42.6487	5.00E-05
S000003426	XKS1		376.122	163.968	5.00E-05
S000001204	YAP1801		503.984	209.729	5.00E-05
S000002667	YAP6		45.4923	94.825	5.00E-05
S000000077	YAR029W		27.4941	12.9156	1.46E-02
S000000080	YAT1		262.302	108.541	5.00E-05
S000000826	YAT2		429.459	51.5926	5.00E-05
S000002146	YBL005W-A		8.4949	3.71772	4.00E-04
S000000124	YBL028C		21.77	58.1043	5.00E-05
S000007591	YBL029C-A		2041.82	834.912	5.00E-05
S000000182	YBL086C		472.98	213.154	5.00E-05
S000028736	YBR056W-A		97.5058	44.9201	1.90E-03
S000028532	YBR072C-A		8.48439	0	1.76E-02
S000028600	YBR126W-A		3246.54	1001.32	5.00E-05
S000000342	YBR138C		30.3317	11.6033	5.00E-05
S000000343	YBR139W		524.747	261.471	5.00E-05
S000087085	YBR201C-A		641.785	291.75	5.00E-05
S000000442	YBR238C		1.62258	4.71849	5.00E-05
S000000488	YBR284W		51.6315	21.7116	5.00E-05
S000000524	YCL019W		10.2903	4.93031	5.00E-05
S000007549	YCL021W-A		29.182	13.3002	2.50E-04
S000000609	YCR016W		6.96217	21.0226	5.00E-05
S000000617	YCR023C		99.6625	48.4379	5.00E-05
S000000699	YCR102C		4.41123	1.87766	3.00E-04
S000003978	YCT1		215.415	516.791	5.00E-05
S000002167	YDL009C		174.75	71.7295	5.55E-03
S000002279	YDL121C		9.67876	28.2261	5.00E-05
S000002342	YDL183C		186.076	87.7361	5.00E-05
S000002358	YDL199C		206.566	78.5133	5.00E-05
S000002449	YDR042C		5.39233	1.02024	5.00E-04
S000007391	YDR098C-B		3.4554	1.69784	5.00E-05
S000002541	YDR134C		8512.1	3586.94	5.00E-05
S000002670	YDR262W		1347.44	466.011	5.00E-05
S000002922	YDR514C		6.68541	20.8112	5.00E-05
S000004239	YEF3		111.337	337.395	5.00E-05
S000000836	YER034W		16.3829	33.1675	5.00E-05
S000000881	YER079W		1874.65	653.886	5.00E-05
S000000886	YER084W		163.285	56.3138	5.00E-05
S000000958	YER156C		9.21267	18.8977	5.00E-05
S000001548	YET1		1491.24	727.107	5.00E-05
S000004643	YET2		231.864	114.331	5.00E-05
S000028547	YFL041W-A		18.3982	38.6523	2.19E-02
S000001843	YFL051C		177.083	86.6296	5.00E-05
S000001840	YFL054C		464.168	228.666	5.00E-05
S000005488	YGK3		117.63	44.0264	5.00E-05
S000002983	YGL015C		4.84784	1.39496	1.16E-02
S000003069	YGL101W		17.4907	35.014	5.00E-05
S000003085	YGL117W		178.345	86.2702	5.00E-05
S000028635	YGL188C-A		0	20.1395	3.10E-03
S000003211	YGL242C		3.66004	18.9481	5.00E-05
S000003249	YGR017W		79.3672	220.723	5.00E-05
S000003250	YGR018C		52.1127	132.777	2.83E-02
S000007407	YGR038C-A		4.63997	0.837486	4.50E-04
S000003354	YGR122W		116.752	58.1186	5.00E-05
S000003381	YGR149W		334.758	158.253	5.00E-05
S000003466	YHB1		69.659	232.986	5.00E-05
S000001000	YHL008C		28.0445	13.8673	5.00E-05
S000001009	YHL017W		7.21022	16.3328	5.00E-05
S000001041	YHL049C		1.60702	0.695823	2.33E-02
S000001064	YHR022C		19.6877	9.72041	1.50E-04
S000028552	YHR086W-A		6.99108	0	4.75E-03

S000001139	YHR097C		1504.99	485.599	5.00E-05
S000007421	YHR214C-C		54.6572	22.9717	5.00E-05
S000028654	YHR214C-E		17.321	3.75098	3.00E-04
S000006122	YIG1		764.282	258.39	5.00E-05
S000001317	YIL055C		90.0212	44.9699	5.00E-05
S000001329	YIL067C		8.92708	26.6708	5.00E-05
S000003643	YJL107C		7.64283	3.08514	2.75E-03
S000003707	YJL171C		68.4293	33.2052	5.00E-05
S000003749	YJL213W		168.601	78.2475	5.00E-05
S000003754	YJL218W		1.5274	10.3096	5.00E-05
S000003876	YJR115W		641.357	220.072	5.00E-05
S000003907	YJR146W		190.928	56.76	5.00E-04
S000001554	YKL071W		61.819	141.798	5.00E-05
S000028667	YKL096C-B		12.7038	0	1.76E-02
S000001731	YKR023W		4.4512	15.4284	5.00E-05
S000003981	YLL058W		4.98183	14.8368	5.00E-05
S000003991	YLR001C		159.114	77.5372	5.00E-05
S000004036	YLR046C		42.3078	123.743	5.00E-05
S000004039	YLR049C		60.41	27.0126	5.00E-05
S000004043	YLR053C		1448.47	111.94	5.00E-05
S000004167	YLR177W		163.341	72.6593	5.00E-05
S000028808	YLR264C-A		0	115.097	1.45E-03
S000004277	YLR287C		16.4901	42.2516	5.00E-05
S000028571	YLR342W-A		5.28407	0	7.50E-03
S000007620	YLR363W-A		13.9162	33.3238	7.00E-04
S000004411	YLR419W		2.74123	8.39784	5.00E-05
S000004438	YLR446W		181.362	79.624	5.00E-05
S000004480	YML018C		21.2843	62.9743	5.00E-05
S000004501	YML037C		0.387588	1.38696	9.05E-03
S000004547	YML082W		3.85377	9.29058	5.00E-05
S000028688	YML100W-A		6.63725	0	1.76E-02
S000028691	YMR001C-A		0	2.57153	2.40E-02
S000004620	YMR018W		13.2928	6.4449	5.00E-05
S000004648	YMR045C		26.1038	11.8899	5.00E-05
S000004689	YMR084W		54.7186	16.5319	5.00E-05
S000004690	YMR085W		98.2912	35.8989	5.00E-05
S000003871	YMR1		3.69096	7.44618	5.00E-05
S000004737	YMR130W		9.3658	22.8656	5.00E-05
S000004752	YMR144W		6.14661	2.86633	5.50E-04
S000004858	YMR244W		5.07841	2.12728	1.00E-04
S000004910	YMR295C		713.256	356.063	5.00E-05
S000005078	YNL134C		2850	952.932	5.00E-05
S000005137	YNL193W		66.686	27.7128	5.00E-05
S000005138	YNL194C		1428.84	306.836	5.00E-05
S000005139	YNL195C		2292.38	687.196	5.00E-05
S000005297	YNR014W		615.596	198.309	5.00E-05
S000005356	YNR073C		46.3152	22.79	5.00E-05
S000005384	YOL024W		3.76763	1.54646	1.19E-02
S000005418	YOL057W		7.31186	17.6988	5.00E-05
S000005467	YOL107W		75.3965	31.0806	5.00E-05
S000007627	YOL159C-A		56.9715	27.3242	2.50E-04
S000005545	YOR019W		291.834	73.8448	5.00E-05
S000028710	YOR032W-A		45.3002	22.0454	1.16E-02
S000028856	YOR034C-A		18.3115	5.72494	4.65E-03
S000005794	YOR268C		39.0224	13.7497	5.00E-05
S000028587	YOR381W-A		5.6025	0	3.10E-03
S000000387	YPC1		799.395	264.351	5.00E-05
S000001899	YPI1		72.6232	152.526	5.00E-05
S000000232	YPK3		5.41894	12.4652	5.00E-05
S000006029	YPL108W		4.91188	11.4212	3.00E-04
S000006178	YPL257W		102.537	49.0574	5.00E-05
S000006181	YPL260W		646.476	295.31	5.00E-05
S000006185	YPL264C		30.7676	13.2655	5.00E-05
S000006207	YPR003C		90.9761	35.3157	5.00E-05
S000122558	YPR010C-A		4289.58	1582.37	5.00E-05
S000006288	YPR084W		21.6304	43.4977	5.00E-05

S000006313	YPR109W		398.016	191.61	5.00E-05
S000113589	YPR145C-A		265.624	104.782	5.00E-05
S000001478	YPS6		79.8653	38.525	5.00E-05
S000005037	YPT53		340.563	147.957	5.00E-05
S000004252	YPT6		23.1029	47.5952	1.00E-04
S000005688	YRR1		43.9225	159.547	5.00E-05
S000004267	YSH1		6.86986	18.004	5.00E-05
S000001761	YSR3		120.074	42.1667	5.00E-05
S000005798	YTM1		6.55785	24.6788	5.00E-05
S000003592	ZAP1		69.4484	17.1727	5.00E-05
S000005469	ZEO1		6603.61	2188.23	5.00E-05
S000001842	ZNF1		175.108	84.7728	5.00E-05
S000005514	ZPS1		57.646	26.4019	5.00E-05
S000003517	ZUO1		40.6006	131.822	5.00E-05

Table 4-A4. FPKM values of the differentially expressed genes in the MS300c-strain.

Gene	Gene short name	1 h			4 h		
		Blank	Exposed	P value	Blank	Exposed	P value
S000005982	ALD6	95.0936	272.721	5.00E-05	131.5	2486.16	5.00E-05
S000000057	BDH2	67.2204	149.082	5.00E-05	245.408	768.798	5.00E-05
S000006032	CAR1	262.042	129.763	5.00E-05	1236.28	300.44	5.00E-05
S000004338	CIS1	26.6995	336.188	5.00E-05	55.6508	3725.58	5.00E-05
S000005511	GRE2	70.5196	176.241	5.00E-05	194.344	420.03	5.00E-05
S000000276	HSP26	69.3121	250.993	5.00E-05	6620.02	18948.8	5.00E-05
S000003752	IMA5	7.66873	27.1922	5.00E-05	5.22659	581.14	5.00E-05
S000006056	ISU1	673.125	1349.52	5.00E-05	1629.19	9553.7	5.00E-05
S000006398	OPT2	16.9695	7.55475	5.00E-05			
S000006092	OYE3	7.23596	18.8137	5.00E-05	32.1437	500.301	5.00E-05
S000002814	PDR15	26.9746	70.7301	5.00E-05	60.347	386.098	5.00E-05
S000005175	PDR16	157.055	377.621	5.00E-05	50.5616	428.774	5.00E-05
S000005679	PDR5	226.4	681.939	5.00E-05	75.8023	1555.9	5.00E-05
S000000500	PHO89	64.6717	30.4929	5.00E-05			
S000004610	PLB1	127.653	319.71	5.00E-05	160.424	813.262	5.00E-05
S000005575	RSB1	104.128	242.104	5.00E-05	76.6106	573.469	5.00E-05
S000006491	SCR1	83.0627	169.871	5.00E-05			
S000003429	SNG1	21.7107	478.289	5.00E-05	42.1152	3754.05	5.00E-05
S000002418	SNQ2	39.8947	542.851	5.00E-05	88.0922	4600.24	5.00E-05
S000087162	snR161	0	8.21063	0.01805			
S000006509	snR190	39.7768	99.0178	0.0003			
S000001318	VHR1	48.7429	122.165	5.00E-05	56.6069	376.027	5.00E-05
S000007399	YDR316W-B	1.43383	0.279713	5.00E-05			
S000003267	YGR035C	35.5075	387.784	5.00E-05	11.653	1595.97	5.00E-05
S000003979	YLL056C	9.85211	98.3876	5.00E-05	31.0434	6927.59	5.00E-05
S000007225	YLR035C-A	2.3501	4.8589	5.00E-05			
S000004036	YLR046C	17.6044	114.205	5.00E-05	26.4125	242.232	5.00E-05
S000004708	YMR102C	41.3945	135.125	5.00E-05	10.5662	72.225	5.00E-05
S000004858	YMR244W	8.09014	4.00641	0.0002			
S000028849	YMR247W-A	14.9655	0	0.01755			
S000003513	YOR1	17.8977	43.1784	5.00E-05	48.3563	478.562	5.00E-05
S000007352	YOR142W-B	0.453453	1.82317	0.0137			
S000005794	YOR268C	2.79684	0.809356	0.01295	32.1555	13.4198	5.00E-05
S000005828	YOR302W	4915.7	0	0.00135			
S000028587	YOR381W-A	0	4.83098	0.0138			
S000006009	YPL088W	50.0949	133.826	5.00E-05	35.1839	331.763	5.00E-05
S000005085	AAH1				12.476	43.2716	5.00E-05
S000005316	ABZ1				56.7368	122.844	5.00E-05
S000000847	ACA1				40.6738	87.8762	5.00E-05
S000004121	ACE2				16.1685	7.28492	5.00E-05
S000006188	ACM1				9.00918	4.04465	0.0006
S000004796	ADD37				75.7702	30.0029	5.00E-05
S000000070	ADE1				225.118	107.73	5.00E-05
S000004727	ADE17				77.8714	37.6966	5.00E-05
S000005446	ADH1				1152.98	2427.52	0.00025
S000004918	ADH2				51.563	15.229	5.00E-05
S000000349	ADH5				73.444	158.767	5.00E-05
S000005327	AGA1				125.273	31.1091	5.00E-05
S000001864	AGX1				67.6531	347.886	5.00E-05
S000000678	AHC2				833.682	364.152	5.00E-05
S000001013	AIM17				1264.33	390.061	5.00E-05
S000001520	AIM26				8.81022	1.72155	0.00285
S000004605	AIM34				24.4422	10.2598	5.00E-05
S000004766	AIM36				117.95	240.969	5.00E-05
S000001341	AIR1				26.4363	64.9431	5.00E-05
S000005862	ALA1				64.925	132.279	5.00E-05
S000004779	ALD3				123.332	444.881	5.00E-05
S000000875	ALD5				38.3445	227.051	5.00E-05
S000000274	ALG14				62.1539	25.6275	5.00E-05
S000000447	ALG7				21.4618	9.15759	5.00E-05
S000000105	ALK2				13.9345	2.54628	5.00E-05

S000000415	AME1		53.1775	18.6725	5.00E-05
S000000362	AMN1		130.76	276.484	5.00E-05
S000003808	ANB1		0.944193	10.7643	0.00395
S000001168	ANS1		4.26795	1.89151	0.01555
S000000555	APA1		64.4215	223.553	5.00E-05
S000005116	APC1		12.8256	3.10116	5.00E-05
S000000355	APD1		337.139	1194.91	5.00E-05
S000001586	APE1		356.522	136.04	5.00E-05
S000005009	AQR1		160.947	65.2259	5.00E-05
S000006396	AQY1		54.7234	144.6	5.00E-05
S000000838	ARB1		102.241	314.903	5.00E-05
S000005419	ARG1		97.1028	608.929	5.00E-05
S000003624	ARG3		21.3436	65.76	5.00E-05
S000003125	ARI1		22.0698	153.915	5.00E-05
S000002788	ARO10		45.412	11.8085	5.00E-05
S000000453	ARO4		16.0721	60.6772	5.00E-05
S000006264	ARO7		26.0965	7.32945	5.00E-05
S000001179	ARO9		106.097	17.0181	5.00E-05
S000002513	ARP10		23.5607	3.35017	5.00E-05
S000002508	ARX1		20.7562	75.7243	5.00E-05
S000004722	ASC1		45.8643	314.929	5.00E-05
S000003706	ASG7		5.27203	2.26773	0.0022
S000001668	ASH1		35.5387	73.8984	5.00E-05
S000001535	ASK1		50.7271	199.347	5.00E-05
S000006349	ASN1		345.862	169.832	5.00E-05
S000002592	ATC1		29.0705	97.118	5.00E-05
S000003148	ATG1		44.5657	18.9253	5.00E-05
S000005678	ATG40		127.597	264.568	5.00E-05
S000006171	ATG41		118.899	320.618	5.00E-05
S000002308	ATG9		50.9292	24.0182	5.00E-05
S000006230	ATH1		123.66	55.9823	5.00E-05
S000004584	ATR1		19.2439	47.034	5.00E-05
S000005537	AUS1		8.03336	17.5656	5.00E-05
S000000790	AVT2		13.1246	4.80718	5.00E-05
S000003456	AZR1		14.3516	60.4982	5.00E-05
S000001251	BAT1		250.38	708.929	5.00E-05
S000006176	BBP1		8.65293	2.44327	5.00E-05
S000001735	BCH2		11.5431	5.53515	5.00E-05
S000004391	BDF1		96.0077	40.7801	5.00E-05
S000005724	BFR1		89.0542	31.1122	5.00E-05
S000002707	BFR2		19.3099	49.2168	5.00E-05
S000005340	BIO4		17.9	6.51062	5.00E-05
S000006138	BMS1		18.4048	47.2334	5.00E-05
S000001358	BMT5		21.7333	43.8426	5.00E-05
S000003786	BNA1		59.6066	225.209	5.00E-05
S000002836	BNA7		28.281	76.9727	5.00E-05
S000005177	BNI4		21.0065	7.72989	5.00E-05
S000001421	BNR1		7.36918	3.29207	5.00E-05
S000001078	BRL1		16.1343	8.02025	5.00E-05
S000000193	BRN1		6.18238	2.24851	5.00E-05
S000002195	BSC1		4.48151	84.5135	5.00E-05
S000002683	BSC2		38.603	170.113	5.00E-05
S000005497	BSC6		49.3804	24.2014	5.00E-05
S000001869	BST1		38.8533	18.2336	5.00E-05
S000003420	BUB1		4.57369	2.17896	5.00E-05
S000003142	BUD13		40.0557	18.6643	5.00E-05
S000000069	BUD14		78.8929	34.836	5.00E-05
S000000755	BUD16		13.6656	36.8206	5.00E-05
S000005604	BUD21		50.9703	126.611	5.00E-05
S000004345	BUD8		14.7985	6.9257	5.00E-05
S000004888	BUL1		38.8959	16.9283	5.00E-05
S000004216	BUR2		40.0942	81.086	5.00E-05
S000001345	CAB2		59.4849	126.752	5.00E-05
S000004570	CAC2		34.8299	8.22739	5.00E-05
S000003268	CAX4		27.9578	78.9938	5.00E-05
S000004165	CBF5		74.8958	237.645	5.00E-05

S000003406	CBP4		668.346	1502.84	5.00E-05
S000004100	CCW12		2456.53	5528.71	5.00E-05
S000004299	CDA2		0.970104	3.15946	0.0006
S000000595	CDC10		117.001	57.7719	5.00E-05
S000001924	CDC14		31.9567	13.6996	5.00E-05
S000004306	CDC3		101.347	29.0235	5.00E-05
S000004603	CDC5		14.2837	4.47058	5.00E-05
S000003730	CDC6		5.27039	1.89881	5.00E-05
S000006081	CDC60		28.6475	139.066	5.00E-05
S000002709	CFT1		25.817	9.98012	5.00E-05
S000002997	CGR1		43.2397	110.633	5.00E-05
S000000569	CHA1		2323.91	863.165	5.00E-05
S000000227	CHS3		27.9439	7.99447	5.00E-05
S000001094	CIC1		36.5032	123.427	5.00E-05
S000004811	CIK1		13.4137	1.99508	5.00E-05
S000005876	CIN1		48.2641	13.3047	5.00E-05
S000003694	CIS3		41.45	15.8543	5.00E-05
S000000598	CIT2		401.997	1188.76	5.00E-05
S000006205	CIT3		27.4582	166.116	5.00E-05
S000005242	CLA4		25.6029	5.96371	5.00E-05
S000006323	CLB2		5.71411	1.64328	5.00E-05
S000004200	CLB4		16.353	7.61991	5.00E-05
S000003183	CLG1		116.39	262.282	5.00E-05
S000004812	CLN1		5.09097	2.30827	0.0001
S000001620	CMC1		410.817	963.454	5.00E-05
S000028514	CMC4		275.473	699.652	5.00E-05
S000004261	CMG1		38.9223	84.0634	5.00E-05
S000002315	CMR1		10.8646	3.7953	5.00E-05
S000006217	CMR3		25.2996	269.918	5.00E-05
S000000359	CNS1		27.0922	63.7474	5.00E-05
S000005324	COQ2		54.7898	24.7688	5.00E-05
S000003932	COX17		1214.64	2866.55	5.00E-05
S000003294	COX18		44.0529	94.7088	5.00E-05
S000001158	COX23		112.51	247.859	5.00E-05
S000003708	CPS1		81.2773	24.9174	5.00E-05
S000003421	CRH1		156.092	51.2122	5.00E-05
S000001532	CSE4		79.3767	36.5422	5.00E-05
S000000682	CSM1		96.683	42.1189	5.00E-05
S000006121	CSM4		20.3446	9.29325	0.0002
S000006328	CTR1		130.767	818.055	5.00E-05
S000004276	CTS1		195.825	592.391	5.00E-05
S000003320	CTT1		346.417	1083.14	5.00E-05
S000004568	CUE4		156.751	43.4789	5.00E-05
S000001579	CWP1		19.3783	7.48515	5.00E-05
S000001956	CWP2		2388.31	1071.81	5.00E-05
S000003809	CYC1		2796.41	1241.37	5.00E-05
S000003387	CYS4		212.069	583.186	5.00E-05
S000001791	DAD2		42.4399	20.5337	0.0002
S000001841	DAK2		33.6472	11.82	5.00E-05
S000001742	DAL80		51.004	11.6368	5.00E-05
S000006091	DAP1		152.094	568.69	5.00E-05
S000003046	DBP3		22.8368	106.798	5.00E-05
S000004266	DBP9		26.2534	57.3743	5.00E-05
S000004784	DDR48		1265.47	631.348	0.00015
S000002182	DIA3		10.0496	29.7193	5.00E-05
S000004119	DIP2		12.1362	32.6425	5.00E-05
S000002333	DLD1		316.448	969.895	5.00E-05
S000000797	DLD3		115.751	284.811	5.00E-05
S000001365	DPH1		24.2458	49.2964	5.00E-05
S000001779	DRE2		467.391	1274.16	5.00E-05
S000000926	DSE1		58.0131	255.919	5.00E-05
S000001186	DSE2		145.525	469.68	5.00E-05
S000005790	DSE3		53.4899	161.971	5.00E-05
S000005350	DSE4		26.897	193.51	5.00E-05
S000001449	DSN1		43.6374	18.3899	5.00E-05
S000000384	DTR1		6.13716	13.4121	5.00E-05

S000003029	DUO1		19.9909	6.77434	5.00E-05
S000001008	DUR3		9.30187	21.4541	5.00E-05
S000004781	EAR1		137.306	62.1761	5.00E-05
S000001655	EBP2		73.5722	184.188	5.00E-05
S000000055	ECM1		15.2458	36.2377	5.00E-05
S000002854	ECM11		4.38174	1.84409	0.0001
S000004735	ECM16		8.27478	21.3515	5.00E-05
S000003737	ECM25		25.5876	12.2433	5.00E-05
S000001022	ECM29		19.0598	8.75642	5.00E-05
S000004428	ECM30		44.0492	21.2568	5.00E-05
S000000282	ECM33		441.06	122.714	5.00E-05
S000001784	ECM4		100.431	374.11	5.00E-05
S000001923	ECO1		12.2802	3.28673	5.00E-05
S000003233	EFM5		33.7893	92.51	5.00E-05
S000002793	EFT2		46.9665	134.14	5.00E-05
S000007525	EGO4		2296.91	6843.27	5.00E-05
S000005271	EGT2		42.4137	164.166	5.00E-05
S000005174	ELA1		24.0846	49.9354	5.00E-05
S000003432	ELP2		17.5178	40.5492	5.00E-05
S000006007	ELP3		22.7201	51.3683	5.00E-05
S000003168	EMP24		234.6	103.354	5.00E-05
S000002447	ENA1		24.7648	8.2249	5.00E-05
S000001217	ENO2		1137.3	164.412	5.00E-05
S000000451	ENP1		30.2752	89.176	5.00E-05
S000003377	ENP2		11.674	27.3889	5.00E-05
S000004652	ERB1		13.4318	43.7314	5.00E-05
S000004595	ERG13		256.027	61.9987	5.00E-05
S000004815	ERG2		135.193	62.05	5.00E-05
S000004467	ERG6		88.7399	31.0389	5.00E-05
S000001937	ERJ5		50.587	24.3475	5.00E-05
S000004599	ERO1		120.676	248.775	5.00E-05
S000000005	ERP2		40.0689	19.3136	5.00E-05
S000004942	ERR3		19.7911	59.3778	5.00E-05
S000003261	ERV1		113.287	232.761	5.00E-05
S000001413	ESL1		30.148	9.10975	5.00E-05
S000005577	ETT1		19.0721	96.1351	5.00E-05
S000005559	EXO1		20.2177	9.28885	5.00E-05
S000001915	FAB1		24.952	10.7614	5.00E-05
S000003693	FAR1		21.9542	4.13229	5.00E-05
S000002747	FCF1		120.937	52.5146	5.00E-05
S000000858	FCY2		215.519	707.889	5.00E-05
S000004938	FET4		28.5342	71.6807	5.00E-05
S000005917	FEX1		2.97822	0.872115	0.0002
S000006200	FEX2		7.19059	2.73165	5.00E-05
S000000244	FIG1		4.923	2.20345	0.00105
S000000685	FIG2		26.8693	11.4757	5.00E-05
S000000834	FIR1		17.4868	5.85124	5.00E-05
S000005909	FIT2		79.5693	270.675	5.00E-05
S000004334	FKS1		73.2475	22.6823	5.00E-05
S000001810	FLO10		12.9661	5.96465	5.00E-05
S000001458	FLO11		4.12959	10.8115	5.00E-05
S000000059	FLO9		11.9935	27.1976	5.00E-05
S000001360	FMC1		188.543	380.619	5.00E-05
S000000984	FMP10		323.392	727.658	5.00E-05
S000000251	FMP23		24.5294	76.6764	5.00E-05
S000004067	FMP25		38.7982	143.26	5.00E-05
S000000109	FMT1		7.61291	1.85367	5.00E-05
S000005200	FOL1		15.972	32.6685	5.00E-05
S000004441	FPR4		44.4185	94.732	5.00E-05
S000005512	FRE7		12.35	36.6785	5.00E-05
S000006062	FRK1		50.1677	16.7988	5.00E-05
S000005851	FRT1		68.3586	23.8457	5.00E-05
S000005797	FSF1		41.0481	95.0636	5.00E-05
S000000532	FUS1		125.113	11.5251	5.00E-05
S000005077	FYV6		137.029	67.3979	5.00E-05
S000003428	FYV8		57.9279	28.0359	5.00E-05

S000001747	GAP1		210.542	13.6483	5.00E-05
S000004924	GAS1		132.232	51.5308	5.00E-05
S000004828	GAS3		25.7979	5.628	5.00E-05
S000005492	GAS4		10.0767	4.72743	5.00E-05
S000005390	GAS5		224.055	81.2658	5.00E-05
S000001873	GAT1		468.834	172.932	5.00E-05
S000004801	GCV2		200.298	34.4745	5.00E-05
S000000042	GCV3		1131.17	564.927	5.00E-05
S000005646	GCY1		610.724	1705.93	5.00E-05
S000006388	GDB1		411.166	168.934	5.00E-05
S000000058	GDH3		164.917	551.97	5.00E-05
S000000748	GEA2		10.1974	4.47817	5.00E-05
S000000541	GFD2		3.26296	10.5828	5.00E-05
S000002717	GIC2		62.8904	7.39123	5.00E-05
S000005097	GIM3		103.863	45.4046	5.00E-05
S000002915	GIN4		5.85073	2.34586	5.00E-05
S000000249	GIP1		9.8326	36.3351	5.00E-05
S000006058	GIP3		36.2293	168.244	5.00E-05
S000002503	GIS1		54.7085	117.159	5.00E-05
S000000737	GLC3		368.401	134.117	5.00E-05
S000000772	GLY1		164.97	370.118	5.00E-05
S000001738	GMH1		61.8515	28.088	5.00E-05
S000001047	GPA1		111.844	41.7464	5.00E-05
S000002180	GPD1		339.153	101.365	5.00E-05
S000004983	GPI15		82.6502	34.6749	5.00E-05
S000002179	GPM2		80.5153	171.882	5.00E-05
S000001315	GPP1		120.732	844.375	5.00E-05
S000001509	GPX1		209.164	659.086	5.00E-05
S000006144	GRE1		124.91	1984.78	5.00E-05
S000003264	GSC2		91.7432	194.659	5.00E-05
S000003639	GSM1		96.9157	45.0503	5.00E-05
S000004284	GSP1		262.527	594.413	5.00E-05
S000003395	GTR2		55.9261	123.541	5.00E-05
S000004830	GUA1		41.4923	245.275	5.00E-05
S000003627	GWT1		31.9206	15.2519	5.00E-05
S000001592	HAP4		725.44	2048.46	5.00E-05
S000004903	HAS1		10.5358	78.3674	5.00E-05
S000000128	HEK2		70.6659	33.6087	5.00E-05
S000005763	HES1		3.0007	6.50134	0.0001
S000003419	HGH1		12.8486	39.0257	5.00E-05
S000000213	HHF1		1830.64	706.495	5.00E-05
S000004975	HHF2		817.091	362.874	5.00E-05
S000000214	HHT1		2393.79	933.448	5.00E-05
S000003423	HIP1		67.4944	181.715	5.00E-05
S000005558	HMS1		31.426	65.0807	5.00E-05
S000000238	HMT1		65.3734	171.704	5.00E-05
S000002713	HNT2		26.5852	55.8223	5.00E-05
S000005784	HNT3		30	67.5986	5.00E-05
S000004635	HOF1		9.86758	3.33514	5.00E-05
S000002565	HOM2		112.082	363.388	5.00E-05
S000000854	HOM3		20.2342	73.0215	5.00E-05
S000003001	HOP2		12.3552	5.18015	5.00E-05
S000006037	HOS3		40.1844	12.102	5.00E-05
S000001567	HOT13		13.9416	72.5678	5.00E-05
S000005483	HRP1		38.4108	83.1706	5.00E-05
S000005546	HSP10		4963.09	11608.9	5.00E-05
S000001880	HSP12		16127.4	38221.6	0.00025
S000003695	HSP150		3783.51	790.562	5.00E-05
S000000099	HTA2		194.126	48.4596	5.00E-05
S000002632	HTB1		2379.16	791.738	5.00E-05
S000000098	HTB2		153.943	38.6752	5.00E-05
S000003797	HUL4		11.9905	5.20356	5.00E-05
S000001949	HXK1		5312.3	11437.4	0.0021
S000001136	HXT1		7.0005	53.1405	5.00E-05
S000005516	HXT11		6.73473	19.1537	5.00E-05
S000001433	HXT12		12.5287	45.9582	5.00E-05

S000001432	HXT12		8.00548	44.4634	5.00E-05
S000004613	HXT2		194.157	788.155	5.00E-05
S000002753	HXT3		561.069	5561.96	5.00E-05
S000001134	HXT4		792.21	3375.73	5.00E-05
S000003750	HXT8		7.32454	94.703	5.00E-05
S000003755	HXT9		3.50071	30.7399	5.00E-05
S000003883	IBA57		51.2433	117.026	5.00E-05
S000000361	ICS2		26.3966	294.799	5.00E-05
S000004089	ICT1		37.8335	99.5561	5.00E-05
S000004808	ICY1		115.123	1268.19	5.00E-05
S000000172	ILS1		48.6246	99.6571	5.00E-05
S000004714	ILV2		246.615	808.108	5.00E-05
S000003777	ILV3		64.6033	516.43	5.00E-05
S000004347	ILV5		406.808	826.714	0.0001
S000005517	IMA2		12.3359	132.732	5.00E-05
S000001259	IMD2		88.7318	11.245	5.00E-05
S000001191	IMP3		23.9156	67.3278	5.00E-05
S000005019	IMP4		47.7713	112.26	5.00E-05
S000001088	INM1		12.0605	31.3892	5.00E-05
S000002530	INO2		47.5696	154.797	5.00E-05
S000004817	INP1		17.1176	6.2498	5.00E-05
S000004773	INP2		17.4018	6.34381	5.00E-05
S000001909	IOC3		42.5733	20.3671	5.00E-05
S000001127	IPI1		11.4382	25.5772	5.00E-05
S000005126	IPI3		11.888	42.0577	5.00E-05
S000006130	IPL1		3.55602	1.43065	0.0002
S000002479	IPT1		93.6241	206.464	5.00E-05
S000003956	IRC19		23.7523	11.757	5.00E-05
S000178119	IRT1		12.4567	190.216	5.00E-05
S000003609	JEM1		15.8479	7.31276	5.00E-05
S000001700	JEN1		102.575	216.845	5.00E-05
S000003858	JJJ3		9.77023	20.8061	0.0001
S000003980	JLP1		14.7656	29.9312	5.00E-05
S000002984	KAP122		15.0813	6.54086	5.00E-05
S000003571	KAR2		1015.91	407.6	5.00E-05
S000006345	KAR3		15.5222	4.96	5.00E-05
S000000560	KAR4		152.045	28.2024	5.00E-05
S000006190	KAR9		18.3731	5.96188	5.00E-05
S000000529	KCC4		9.93023	4.64771	5.00E-05
S000003815	KCH1		16.1635	7.77484	5.00E-05
S000006184	KEL3		17.3628	5.34022	5.00E-05
S000002529	KIN1		34.9284	14.0282	5.00E-05
S000000159	KIP1		6.5653	1.89266	5.00E-05
S000006076	KIP2		16.4841	5.20968	5.00E-05
S000003184	KIP3		25.8056	12.825	5.00E-05
S000006363	KRE6		76.756	25.5075	5.00E-05
S000002444	KRS1		83.8721	311.33	5.00E-05
S000005974	KTR6		87.9457	39.3185	5.00E-05
S000001491	LAC1		70.0484	196.083	5.00E-05
S000001198	LAM1		26.1311	11.0548	5.00E-05
S000004250	LCB5		83.9425	41.7414	5.00E-05
S000000929	LCP5		21.0026	65.596	5.00E-05
S000002977	LEU1		421.733	1631.78	5.00E-05
S000000523	LEU2		342.647	2024.46	5.00E-05
S000005048	LEU4		237.477	487.925	5.00E-05
S000005634	LEU9		5.40389	18.6391	5.00E-05
S000003831	LIA1		44.7315	118.753	5.00E-05
S000004913	LIP1		104.189	255.77	5.00E-05
S000003930	LMO1		16.0068	6.52526	5.00E-05
S000002399	LRG1		10.214	2.83871	5.00E-05
S000005291	LRO1		84.8299	32.8449	5.00E-05
S000001123	LRP1		70.0649	151.257	5.00E-05
S000003783	LSM8		32.4906	6.43695	5.00E-05
S000000022	LTE1		6.729	1.67171	5.00E-05
S000001473	LYS1		209.167	55.5641	5.00E-05
S000002341	LYS20		45.3767	145.228	5.00E-05

S000002289	LYS21		52.0434	119.938	5.00E-05
S000001512	MAE1		38.2782	167.375	5.00E-05
S000000023	MAK16		21.8212	59.8269	5.00E-05
S000000346	MAK5		21.8171	51.7938	5.00E-05
S000003524	MAL12		16.4925	70.5399	5.00E-05
S000000908	MAM1		3.43509	1.47052	0.00165
S000001332	MAM33		233.207	556.59	5.00E-05
S000000119	MCM2		13.8373	5.5225	5.00E-05
S000000758	MCM3		34.53	15.7726	5.00E-05
S000004264	MCM5		20.6127	8.10044	5.00E-05
S000005486	MDH2		1898.52	480.722	5.00E-05
S000000340	MEC1		11.9294	5.66292	5.00E-05
S000005700	MED4		33.8346	67.8615	5.00E-05
S000005878	MEK1		6.67348	2.91509	5.00E-05
S000003496	MES1		34.9473	97.6368	5.00E-05
S000004294	MET17		46.0842	95.5842	5.00E-05
S000001390	MET18		17.7212	5.65715	5.00E-05
S000005425	MET22		27.0045	57.0196	5.00E-05
S000003898	MET5		33.4859	16.6329	5.00E-05
S000000893	MET6		177.58	391.674	5.00E-05
S000006108	MF(ALPHA)1		1229.29	417.576	5.00E-05
S000003481	MGA1		17.214	54.0132	5.00E-05
S000005758	MGE1		189.551	417.379	5.00E-05
S000005162	MGS1		9.11322	4.39392	5.00E-05
S000028520	MHF2		54.1455	174.616	5.00E-05
S000001724	MIC60		210.973	73.7611	5.00E-05
S000001572	MIF2		13.3123	3.99716	5.00E-05
S000004789	MMT1		16.3889	6.33619	5.00E-05
S000003151	MND1		2.52699	5.64066	0.00185
S000004047	MNL2		27.4829	11.0176	5.00E-05
S000006003	MOT1		20.3895	4.38302	5.00E-05
S000004674	MOT3		69.6253	34.8055	5.00E-05
S000005814	MPD1		58.0664	21.9998	5.00E-05
S000002186	MPS1		39.9199	19.5255	5.00E-05
S000003146	MPT5		68.7948	30.5079	5.00E-05
S000003111	MRF1		64.5538	157.429	5.00E-05
S000002440	MRH1		216.334	87.1103	5.00E-05
S000001650	MRP49		288.246	629.703	5.00E-05
S000004806	MRPL24		156.64	318.526	5.00E-05
S000001653	MRPL38		181.072	519.328	5.00E-05
S000001190	MRPL6		229.424	475.884	5.00E-05
S000005250	MRPS18		177.983	438.825	5.00E-05
S000005897	MRS6		71.2533	232.587	5.00E-05
S000001492	MRT4		69.6101	256.02	5.00E-05
S000002690	MRX10		63.0002	169.11	5.00E-05
S000002744	MRX8		21.2305	49.6293	5.00E-05
S000005592	MSA1		42.8654	12.0015	5.00E-05
S000001785	MSA2		25.7207	6.88774	5.00E-05
S000003246	MSB2		69.6035	10.1632	5.00E-05
S000005393	MSE1		26.296	74.5013	5.00E-05
S000005450	MSH2		8.06358	1.72659	5.00E-05
S000002685	MTH1		279.31	761.898	5.00E-05
S000003586	MTR4		13.9578	40.1377	5.00E-05
S000005824	MUM3		6.40298	1.60704	5.00E-05
S000005326	MVD1		208.986	52.5619	5.00E-05
S000001065	MYO1		8.58589	3.03979	5.00E-05
S000004685	NAM7		23.152	50.1584	5.00E-05
S000001128	NAM8		79.2878	28.0701	5.00E-05
S000006047	NAN1		26.4616	70.9238	5.00E-05
S000004981	NCE103		2850.8	581.987	5.00E-05
S000005063	NCS2		19.8499	44.0964	5.00E-05
S000006147	NEW1		14.0031	63.002	5.00E-05
S000002157	NHP6B		443.843	1031.1	5.00E-05
S000004926	NIP1		42.1691	92.5323	5.00E-05
S000006132	NIP7		29.7868	63.6828	5.00E-05
S000001213	NMD3		40.97	120.704	5.00E-05

S000007436	NME1		23.0369	83.4334	5.00E-05
S000005732	NOC2		16.6634	82.7245	5.00E-05
S000006014	NOG1		22.9282	140.267	5.00E-05
S000005336	NOG2		31.6056	134.094	5.00E-05
S000002172	NOP1		69.1578	232.194	5.00E-05
S000005401	NOP12		27.1678	88.4997	5.00E-05
S000005119	NOP13		20.9192	43.6635	5.00E-05
S000002307	NOP14		14.7338	32.3821	5.00E-05
S000005054	NOP15		55.0868	153.237	5.00E-05
S000005005	NOP2		33.8358	93.2796	5.00E-05
S000005964	NOP4		15.4845	51.2566	5.00E-05
S000006067	NOP53		44.1138	103.242	5.00E-05
S000004187	NOP56		49.9823	123.654	5.00E-05
S000005837	NOP58		37.2616	146.84	5.00E-05
S000003547	NOP9		12.6299	29.4315	5.00E-05
S000002840	NPL3		1057.06	486.182	5.00E-05
S000005195	NRD1		43.7308	18.4421	5.00E-05
S000005292	NRM1		8.89891	2.13623	5.00E-05
S000002326	NRP1		13.648	32.7767	5.00E-05
S000000928	NSA2		41.3426	110.235	5.00E-05
S000002263	NSE4		19.0243	9.49154	0.0001
S000003391	NSR1		54.005	455.95	5.00E-05
S000004524	NTE1		31.2686	3.67069	5.00E-05
S000000808	NUG1		31.5404	66.4337	5.00E-05
S000001551	NUP100		31.2871	84.309	5.00E-05
S000002352	NUS1		86.1983	40.2664	5.00E-05
S000001603	OAC1		126.933	348.655	5.00E-05
S000003411	OKP1		18.3542	6.45943	5.00E-05
S000003023	OLE1		149.127	472.843	5.00E-05
S000003748	OPT1		10.9192	44.0227	5.00E-05
S000005205	ORC5		20.9358	10.2401	5.00E-05
S000006117	OXR1		150.281	330.649	5.00E-05
S000000967	PAB1		192.833	453.505	5.00E-05
S000002946	PAD1		72.7986	28.6785	5.00E-05
S000004786	PAI3		695.07	4615.57	5.00E-05
S000002756	PAL1		59.0876	25.7019	5.00E-05
S000001773	PAM17		175.124	361.629	5.00E-05
S000005475	PAP2		21.0038	9.05942	5.00E-05
S000003948	PAU17		4.33179	16.2513	5.00E-05
S000000775	PAU2		27.91	60.6733	5.00E-05
S000000701	PAU3		1.74606	0	5.00E-05
S000006193	PBI1		17.2684	5.65288	5.00E-05
S000000437	PBP2		7.64015	3.55665	0.0001
S000005233	PCL1		2.57142	0.640143	0.0009
S000002285	PCL2		33.1	16.5422	5.00E-05
S000002338	PCL9		23.9932	53.1283	5.00E-05
S000005887	PDE2		70.35	164.39	5.00E-05
S000006206	PDH1		100.573	308.93	5.00E-05
S000000101	PDR3		24.7926	105.734	5.00E-05
S000002520	PDS1		26.4718	10.6701	5.00E-05
S000000640	PER1		53.4134	21.5943	5.00E-05
S000005684	PET123		204.459	432.825	5.00E-05
S000003560	PET130		39.3241	82.1002	5.00E-05
S000005444	PHM7		52.4497	19.1383	5.00E-05
S000000296	PHO3		24.0795	7.90619	5.00E-05
S000004592	PHO84		121.242	1057.9	5.00E-05
S000005913	PHR1		95.7698	45.6576	5.00E-05
S000002991	PIB2		73.8727	29.6758	5.00E-05
S000005630	PIN2		29.1277	9.45366	5.00E-05
S000001647	PIR1		145.926	333.373	5.00E-05
S000001646	PIR3		1035.6	476.752	5.00E-05
S000006317	PIS1		608.575	216.784	5.00E-05
S000002898	PKH1		55.2124	27.1854	5.00E-05
S000002103	PMP2		955.798	2259.82	0.00015
S000005026	PMS1		10.4235	4.81303	5.00E-05
S000000021	PMT2		59.7448	26.8545	5.00E-05

S000006065	POC4		31.1172	14.0475	5.00E-05
S000000292	POL30		21.6007	5.49852	5.00E-05
S000000114	POP8		24.6828	63.5305	5.00E-05
S000004880	PPA2		116.61	270.07	5.00E-05
S000002482	PPH3		15.745	47.9207	5.00E-05
S000005501	PPM2		4.58671	10.8269	5.00E-05
S000004004	PPR1		10.0871	21.1117	5.00E-05
S000000786	PRB1		1393.21	670.101	0.00035
S000005223	PRM1		25.8489	9.30385	5.00E-05
S000003644	PRM10		23.1892	8.05367	5.00E-05
S000006077	PRM4		85.5101	37.6966	5.00E-05
S000001379	PRM5		208.828	65.5823	5.00E-05
S000004510	PRM6		5.0412	1.34683	5.00E-05
S000002197	PRM7		4.1899	59.4462	5.00E-05
S000003088	PRP43		9.78006	39.9279	5.00E-05
S000001664	PRS1		82.0905	192.781	5.00E-05
S000001003	PRS3		82.7172	167.236	5.00E-05
S000005888	PRT1		46.9156	98.4365	5.00E-05
S000003615	PRY1		323.524	100.257	5.00E-05
S000002213	PSA1		98.8268	393.824	5.00E-05
S000005113	PSD1		80.5285	22.4749	5.00E-05
S000005405	PSK2		42.2814	19.0732	5.00E-05
S000004368	PSY3		15.6636	6.88356	5.00E-05
S000000142	PSY4		89.537	39.8786	5.00E-05
S000000329	PTC4		29.2701	80.2697	5.00E-05
S000005474	PTH4		72.1941	10.0089	5.00E-05
S000003820	PTK2		159.238	69.0121	5.00E-05
S000002904	PUF6		23.2303	105.017	5.00E-05
S000000987	PUG1		8.01036	32.8415	5.00E-05
S000004406	PUN1		258.935	43.22	5.00E-05
S000004132	PUT1		840.847	402.761	0.00015
S000005875	PUT4		373.821	126.415	5.00E-05
S000004186	PWP1		25.6914	67.3638	5.00E-05
S000000653	PWP2		9.35801	33.5297	5.00E-05
S000001798	PXL1		19.2455	7.96898	5.00E-05
S000003512	PXR1		79.9085	361.861	5.00E-05
S000003030	PYC1		332.605	1008.12	5.00E-05
S000000422	PYC2		357.848	165.893	5.00E-05
S000000318	RAD16		43.1272	104.458	5.00E-05
S000001596	RAD27		17.8002	7.63818	5.00E-05
S000000897	RAD51		118.97	57.4288	5.00E-05
S000006074	RAD53		4.7052	1.11798	5.00E-05
S000005627	RAS1		19.9019	63.3776	5.00E-05
S000004074	RAX2		14.9572	5.0538	5.00E-05
S000002935	RBA50		97.9517	216.707	5.00E-05
S000000034	RBG1		29.4857	68.7888	5.00E-05
S000004887	RCE1		15.3155	6.26827	5.00E-05
S000004492	RCF1		308.121	668.954	5.00E-05
S000003126	RCK1		2.51662	41.3871	5.00E-05
S000000277	RDH54		22.9848	8.58233	5.00E-05
S000006298	RDS3		68.0809	142.478	5.00E-05
S000003753	REE1		129.622	697.192	5.00E-05
S000000254	REG2		56.9298	295.187	5.00E-05
S000000471	REI1		40.7168	90.498	5.00E-05
S000000507	RER1		271.573	74.5328	5.00E-05
S000005440	REX4		9.81396	21.9936	5.00E-05
S000000065	RFA1		42.8249	16.5337	5.00E-05
S000004063	RFU1		15.1367	71.0754	5.00E-05
S000005653	RGA1		48.417	20.9411	5.00E-05
S000002787	RGA2		28.6572	11.3594	5.00E-05
S000001521	RGT1		81.1776	35.2217	5.00E-05
S000002297	RGT2		51.4367	18.9141	5.00E-05
S000005034	RHO2		43.6388	19.6068	5.00E-05
S000001240	RIX1		5.22752	17.8633	5.00E-05
S000005621	RKI1		14.4066	36.6213	5.00E-05
S000006129	RKM1		16.7614	7.3132	5.00E-05

S000004127	RKM5		10.9038	24.3022	5.00E-05
S000003999	RLP24		58.2707	164.197	5.00E-05
S000004947	RLP7		80.5996	178.41	5.00E-05
S000003276	RME1		113.515	350.397	5.00E-05
S000002873	RMT2		34.2057	95.1771	5.00E-05
S000005016	RNH201		26.1074	67.4016	5.00E-05
S000003969	RNP1		9.35842	2.46408	5.00E-05
S000000872	RNR1		7.67997	1.78596	5.00E-05
S000004852	RNT1		18.2991	46.9749	5.00E-05
S000005544	ROD1		45.9833	21.5267	5.00E-05
S000003302	ROM1		80.4367	38.114	5.00E-05
S000006214	RPA135		14.541	62.5472	5.00E-05
S000005868	RPA190		10.5424	33.0709	5.00E-05
S000003684	RPA34		44.557	128.665	5.00E-05
S000005192	RPA49		20.0481	48.1018	5.00E-05
S000000358	RPB5		54.1712	165.99	5.00E-05
S000001789	RPF2		39.3106	82.9841	5.00E-05
S000004065	RPL10		429.336	1433.44	5.00E-05
S000006306	RPL11A		71.0908	199.434	5.00E-05
S000003317	RPL11B		81.0433	284.136	5.00E-05
S000000780	RPL12A		96.6447	429.111	5.00E-05
S000002826	RPL12B		132.386	424.992	5.00E-05
S000002240	RPL13A		82.3828	253.959	5.00E-05
S000004750	RPL13B		157.854	610.479	5.00E-05
S000001489	RPL14A		77.695	431.324	5.00E-05
S000000993	RPL14B		200.101	601.943	5.00E-05
S000004019	RPL15A		120.629	472.009	5.00E-05
S000001395	RPL16A		69.247	481.818	5.00E-05
S000005013	RPL16B		104.305	374.693	5.00E-05
S000001663	RPL17A		102.456	490.422	5.00E-05
S000003713	RPL17B		64.3877	272.946	5.00E-05
S000005480	RPL18A		84.6612	661.456	5.00E-05
S000002156	RPL19A		172.454	1000.86	5.00E-05
S000000123	RPL19B		188.965	1098.07	5.00E-05
S000003103	RPL1B		87.1402	373.445	5.00E-05
S000004855	RPL20A		92.381	431.033	5.00E-05
S000005839	RPL20B		106.218	595.971	5.00E-05
S000000395	RPL21A		71.2609	469.033	5.00E-05
S000006000	RPL21B		89.2665	405.116	5.00E-05
S000004051	RPL22A		64.8788	404.527	5.00E-05
S000006436	RPL22B		22.4868	140.636	5.00E-05
S000000183	RPL23A		186.461	456.043	5.00E-05
S000000919	RPL23B		129.288	653.585	5.00E-05
S000002999	RPL24A		87.2887	447.828	5.00E-05
S000003380	RPL24B		168.196	464.893	5.00E-05
S000005487	RPL25		173.126	1105.75	5.00E-05
S000004336	RPL26A		199.119	569.401	5.00E-05
S000003266	RPL26B		119.121	478.634	5.00E-05
S000001052	RPL27A		135.022	557.002	5.00E-05
S000002879	RPL27B		90.9473	487.708	5.00E-05
S000006437	RPL29		470.384	1765.56	5.00E-05
S000002104	RPL2A		49.1895	370.437	5.00E-05
S000001280	RPL2B		105.54	502.002	5.00E-05
S000005589	RPL3		248.798	1024.52	5.00E-05
S000002998	RPL30		198.702	921.092	5.00E-05
S000002233	RPL31A		139.161	951.593	5.00E-05
S000004398	RPL31B		78.7361	421.16	5.00E-05
S000000188	RPL32		215.257	1237.42	5.00E-05
S000006064	RPL33A		245.561	698.664	5.00E-05
S000005760	RPL33B		67.7203	603.646	5.00E-05
S000002135	RPL34A		128.959	470.568	5.00E-05
S000001314	RPL34B		174.397	460.408	5.00E-05
S000002350	RPL35A		149.912	560.704	5.00E-05
S000002295	RPL35B		113.249	311.64	5.00E-05
S000004807	RPL36A		147.139	652.094	5.00E-05
S000006438	RPL36B		178.695	793.539	5.00E-05

S000004175	RPL37A		118.526	754.395	5.00E-05
S000002908	RPL37B		474.519	1344.77	5.00E-05
S000004317	RPL38		286.253	742.366	5.00E-05
S000003725	RPL39		687.759	2675.6	5.00E-05
S000001410	RPL40A		306.706	1189.61	5.00E-05
S000001802	RPL40B		152.566	711.978	5.00E-05
S000005106	RPL42A		159.627	1105.26	5.00E-05
S000001183	RPL42B		200.983	1062.8	5.00E-05
S000006247	RPL43A		203.845	1368.96	5.00E-05
S000003855	RPL43B		206.752	492.086	5.00E-05
S000002419	RPL4B		45.1741	191.724	5.00E-05
S000006052	RPL5		96.8415	651.934	5.00E-05
S000004538	RPL6A		71.0709	428.992	5.00E-05
S000004440	RPL6B		31.9513	206.393	5.00E-05
S000006119	RPL7B		20.968	91.7305	5.00E-05
S000001025	RPL8A		73.6667	655.577	5.00E-05
S000003968	RPL8B		91.2754	489.667	5.00E-05
S000003115	RPL9A		29.0332	82.3521	5.00E-05
S000004332	RPP0		94.2064	288.252	5.00E-05
S000002239	RPP1A		228.728	588	5.00E-05
S000002288	RPP1B		134.373	475.363	5.00E-05
S000005399	RPP2A		98.4652	380.821	5.00E-05
S000003446	RPS0A		56.2982	373.162	5.00E-05
S000004038	RPS0B		98.2245	423.754	5.00E-05
S000005819	RPS10A		166.007	617.327	5.00E-05
S000004843	RPS10B		182.097	523.892	5.00E-05
S000002432	RPS11A		131.431	864.591	5.00E-05
S000000252	RPS11B		89.8237	317.855	5.00E-05
S000005896	RPS12		157.326	657.1	5.00E-05
S000002471	RPS13		117.788	505.484	5.00E-05
S000000627	RPS14A		326.62	1234.25	5.00E-05
S000003727	RPS14B		107.297	638.79	5.00E-05
S000005400	RPS15		232.41	683.969	5.00E-05
S000004751	RPS16A		106.285	428.65	5.00E-05
S000002241	RPS16B		74.0354	447.898	5.00E-05
S000004486	RPS17A		172.656	611.054	5.00E-05
S000002855	RPS17B		66.661	344.953	5.00E-05
S000002858	RPS18A		299.752	622.979	5.00E-05
S000004488	RPS18B		89.645	522.524	5.00E-05
S000005481	RPS19A		105.397	388.196	5.00E-05
S000005246	RPS19B		93.723	551.783	5.00E-05
S000004433	RPS1A		115.095	569.809	5.00E-05
S000004528	RPS1B		73.8621	650.407	5.00E-05
S000003091	RPS2		118.232	554.325	5.00E-05
S000001007	RPS20		167.442	786.327	5.00E-05
S000001765	RPS21A		128.808	269.047	5.00E-05
S000003672	RPS21B		179.131	889.004	5.00E-05
S000003726	RPS22A		48.649	263.55	5.00E-05
S000004359	RPS22B		34.7113	272.617	5.00E-05
S000003350	RPS23A		322.93	1343.7	5.00E-05
S000006336	RPS23B		267.343	889.454	5.00E-05
S000000876	RPS24A		127.513	763.736	5.00E-05
S000001331	RPS24B		59.4381	418.844	5.00E-05
S000003259	RPS25A		201.463	757.529	5.00E-05
S000004325	RPS25B		199.612	463.029	5.00E-05
S000003157	RPS26A		317.847	1423.08	5.00E-05
S000000933	RPS26B		37.4883	221.563	5.00E-05
S000001639	RPS27A		296.114	1330.02	5.00E-05
S000001063	RPS27B		251.028	1194.86	5.00E-05
S000004254	RPS28B		187.117	703.692	5.00E-05
S000004380	RPS29A		110.239	318.152	5.00E-05
S000002219	RPS29B		384.175	1332.15	5.00E-05
S000005122	RPS3		177.522	830.693	5.00E-05
S000004278	RPS30A		785.208	1816.67	5.00E-05
S000005708	RPS30B		637.141	3060.56	5.00E-05
S000004157	RPS31		263.147	1065.41	5.00E-05

S000003906	RPS4A		100.707	531.775	5.00E-05
S000001246	RPS4B		82.3673	497.937	5.00E-05
S000003884	RPS5		146.372	969.905	5.00E-05
S000006011	RPS6A		72.0134	342.824	5.00E-05
S000000385	RPS6B		57.9575	263.775	5.00E-05
S000005622	RPS7A		67.4657	397.898	5.00E-05
S000005040	RPS7B		85.0018	269.841	5.00E-05
S000000168	RPS8A		59.3977	198.132	5.00E-05
S000000904	RPS8B		22.5256	152.188	5.00E-05
S000006002	RPS9A		57.12	278.372	5.00E-05
S000000393	RPS9B		45.4546	360.291	5.00E-05
S000004738	RRB1		27.8722	119.282	5.00E-05
S000001080	RRF1		47.0174	131.437	5.00E-05
S000002472	RRG1		18.9031	46.1018	5.00E-05
S000005933	RRP12		7.80527	55.772	5.00E-05
S000000631	RRP43		59.9203	152.394	5.00E-05
S000004842	RRP5		8.84746	39.4307	5.00E-05
S000006341	RRP9		18.9262	43.3645	5.00E-05
S000000668	RSA4		8.38424	27.3551	5.00E-05
S000003888	RSF2		64.4213	26.9306	5.00E-05
S000003384	RSR1		26.4083	12.3889	5.00E-05
S000000199	RTG3		35.1288	70.4891	5.00E-05
S000003393	RTS3		426.585	991.951	5.00E-05
S000006104	RTT10		7.7936	24.7346	5.00E-05
S000003143	SAE2		11.9703	5.32438	5.00E-05
S000004170	SAM1		42.5376	89.428	5.00E-05
S000002312	SAS10		34.7197	84.9663	5.00E-05
S000000601	SAT4		65.1489	169.73	5.00E-05
S000004827	SCJ1		43.4378	19.1788	5.00E-05
S000000241	SCO1		124.095	421.62	5.00E-05
S000004885	SCS7		359.093	859.067	5.00E-05
S000004921	SCW10		80.1034	11.0142	5.00E-05
S000002996	SCW11		38.9661	193.521	5.00E-05
S000003511	SCW4		87.5935	40.8847	5.00E-05
S000003477	SDA1		20.8685	49.2159	5.00E-05
S000000783	SDD1		36.9129	128.468	5.00E-05
S000002919	SDH7		427.485	909.683	5.00E-05
S000004012	SDO1		19.6508	66.7577	5.00E-05
S000001375	SDP1		47.6298	23.2926	5.00E-05
S000000375	SEC66		71.2824	35.2841	5.00E-05
S000002484	SED1		8048.05	3848.85	0.00135
S000000066	SEN34		3.46657	1.60273	0.004
S000003704	SET2		8.52558	17.4546	5.00E-05
S000004994	SFB2		13.7321	6.38551	5.00E-05
S000005842	SFG1		10.7453	3.55097	5.00E-05
S000004313	SFH1		177.703	484.136	5.00E-05
S000001534	SFK1		104.789	484.855	5.00E-05
S000002101	SFT1		99.7876	214.682	5.00E-05
S000001361	SGA1		86.9348	23.8685	5.00E-05
S000004802	SGS1		20.3013	7.30734	5.00E-05
S000001751	SHB17		19.7887	47.0139	5.00E-05
S000000127	SHE1		7.32827	2.29326	5.00E-05
S000004724	SHH3		50.5089	163.937	5.00E-05
S000004048	SHM2		427.588	200.768	5.00E-05
S000002384	SHS1		56.5334	28.1139	5.00E-05
S000001385	SIM1		76.1277	21.0997	5.00E-05
S000004787	SIP18		245.11	9267.85	5.00E-05
S000000791	SIT1		111.306	38.1675	5.00E-05
S000001192	SKG6		10.7061	3.55746	5.00E-05
S000005602	SKI7		34.6872	9.8223	5.00E-05
S000005473	SKM1		63.3921	24.1272	5.00E-05
S000003375	SKN1		81.2154	39.9868	5.00E-05
S000005947	SKS1		219.286	441.837	5.00E-05
S000005187	SLA2		44.737	11.8948	5.00E-05
S000002923	SLF1		52.7005	25.8313	5.00E-05
S000000360	SLI15		19.5274	5.18942	5.00E-05

S000005721	SLK19		26.6303	7.54402	5.00E-05
S000004129	SLS1		38.7416	19.264	5.00E-05
S000003313	SLX9		33.7927	83.6845	5.00E-05
S000005948	SMA1		3.60189	7.79083	0.0006
S000001886	SMC1		10.9963	3.39778	5.00E-05
S000005394	SMC5		16.1584	6.40673	5.00E-05
S000002885	SNF1		71.9659	144.983	5.00E-05
S000005278	SNO2		13.068	5.16198	5.00E-05
S000001834	SNO3		11.2645	4.27147	5.00E-05
S000007499	snR10		260.752	62.9428	5.00E-05
S000007293	snR11		130.445	323.807	5.00E-05
S000007295	snR19		28.6697	101.695	5.00E-05
S000007297	snR32		75.5651	20.3702	0.00115
S000006500	snR34		48.1256	23.6973	0.0149
S000007299	snR35		245.695	61.006	5.00E-05
S000007300	snR36		93.2153	11.1119	0.00945
S000006501	snR37		92.8086	23.7722	5.00E-05
S000006502	snR42		130.783	65.102	5.00E-05
S000006503	snR43		177.324	25.6569	5.00E-05
S000006505	snR45		144.63	22.7705	0.00065
S000007291	snR5		224.107	54.9538	5.00E-05
S000006454	snR63		29.2628	13.5307	0.00545
S000006461	snR70		101.857	236.048	0.0011
S000006497	snR8		169.036	37.2145	5.00E-05
S000028467	snR82		518.804	77.1578	5.00E-05
S000003099	SNT2		37.3306	18.3451	5.00E-05
S000000752	SNU13		80.4873	598.729	5.00E-05
S000003573	SNX4		170.53	79.7997	5.00E-05
S000003865	SOD1		3641.35	9064.8	5.00E-05
S000004618	SOK2		28.1752	76.5113	5.00E-05
S000001206	SOL3		26.149	54.7584	5.00E-05
S000003920	SOR1		1.28337	0.412309	0.0101
S000002405	SOR2		1.36374	0.512604	0.0121
S000003944	SPA2		14.7387	7.22696	5.00E-05
S000000559	SPB1		9.18879	33.3319	5.00E-05
S000003770	SPC1		81.1322	37.5227	5.00E-05
S000002764	SPC110		8.26864	3.42855	5.00E-05
S000004723	SPC24		13.4474	3.24413	5.00E-05
S000006045	SPC29		11.6599	4.7652	5.00E-05
S000001215	SPC97		5.4724	2.57679	5.00E-05
S000003468	SPG1		466.508	1476.34	5.00E-05
S000004305	SPH1		5.01533	1.14101	5.00E-05
S000001739	SPO14		33.6678	15.253	5.00E-05
S000028425	SPO24		7137.23	22565.4	5.00E-05
S000003928	SPO75		9.50054	28.5856	5.00E-05
S000002930	SPS2		9.82047	4.76158	0.0001
S000000553	SPS22		13.1651	5.743	5.00E-05
S000004791	SPT21		11.9932	4.78538	5.00E-05
S000000285	SPT7		35.1992	17.363	5.00E-05
S000001451	SQT1		39.9592	87.8703	5.00E-05
S000029010	SRG1		1175.26	207.112	5.00E-05
S000001799	SRL3		143.449	49.0125	5.00E-05
S000000542	SRO9		3.00042	9.71543	5.00E-05
S000002700	SRP101		33.108	67.4109	5.00E-05
S000004707	SRT1		7.54019	2.77417	5.00E-05
S000001569	SRX1		82.6015	28.462	5.00E-05
S000000905	SSA4		800.613	341.11	5.00E-05
S000002388	SSB1		54.0466	220.895	5.00E-05
S000005153	SSB2		90.5539	423.432	5.00E-05
S000001108	SSF1		11.5189	29.4722	5.00E-05
S000004444	SST2		61.5649	18.8619	5.00E-05
S000006013	SSU1		94.5178	349.633	5.00E-05
S000004657	STB2		17.7317	6.06115	5.00E-05
S000002576	STB3		197.072	89.2573	5.00E-05
S000001555	STB6		20.305	9.37873	5.00E-05
S000001126	STE12		30.2535	8.89575	5.00E-05

S000002818	STE14		34.8715	16.577	5.00E-05
S000003846	STE18		129.459	266.343	5.00E-05
S000001661	STE3		245.886	84.3664	5.00E-05
S000003240	STF2		2555.25	5240.95	5.00E-05
S000004140	STM1		103.905	456.751	5.00E-05
S000002206	STP4		219.66	1032.53	5.00E-05
S000003152	STR3		13.3319	33.3156	5.00E-05
S000004035	STU2		18.8422	8.57318	5.00E-05
S000005978	SUR1		200.396	430.902	5.00E-05
S000002705	SUR2		94.391	231.696	5.00E-05
S000004516	SUR7		174.672	29.8395	5.00E-05
S000028510	SUS1		119.867	329.4	5.00E-05
S000003130	SUT1		23.8769	119.3	5.00E-05
S000000913	SWI4		12.1425	3.59477	5.00E-05
S000002553	SWI5		15.5686	6.83341	5.00E-05
S000004172	SWI6		57.5929	22.0023	5.00E-05
S000002742	SWR1		44.2818	13.662	5.00E-05
S000002221	SYO1		11.3465	53.2476	5.00E-05
S000003201	TAN1		21.4903	43.2478	5.00E-05
S000001391	TAO3		25.1536	11.2779	5.00E-05
S000001045	TCD1		26.1415	56.2014	5.00E-05
S000004905	TDA1		56.0374	160.104	5.00E-05
S000003769	TDH2		313.582	78.3417	5.00E-05
S000000287	TEC1		365.357	145.191	5.00E-05
S000000271	TIP1		2287.26	749.389	5.00E-05
S000000915	TMN3		31.3259	14.384	5.00E-05
S000003492	TNA1		381.894	144.681	5.00E-05
S000005014	TOM7		274.472	605.575	5.00E-05
S000003827	TOR1		30.06	12.9089	5.00E-05
S000000366	TOS1		122.62	55.6383	5.00E-05
S000003064	TOS8		41.4998	88.3493	5.00E-05
S000005453	TRM10		14.5041	32.2086	5.00E-05
S000005484	TRM11		5.78162	27.5879	5.00E-05
S000005951	TRM44		14.3309	28.8141	5.00E-05
S000001112	TRM5		19.9296	43.8379	5.00E-05
S000002360	TRM8		35.3371	71.2454	5.00E-05
S000002572	TRM82		17.7158	50.7496	5.00E-05
S000002815	TRS120		16.6722	5.48453	5.00E-05
S000002861	TSA2		82.6619	386.215	5.00E-05
S000004566	TSL1		824.409	216.892	5.00E-05
S000002218	TSR1		18.3475	56.3023	5.00E-05
S000004202	TUB4		6.0996	2.51076	5.00E-05
S000001517	TUL1		24.7361	65.2461	5.00E-05
S000002507	TVP15		63.3055	135.08	5.00E-05
S000003018	TYW3		92.8747	43.0393	5.00E-05
S000000900	UBP9		68.4375	31.3288	5.00E-05
S000001518	UGP1		577.974	162.718	5.00E-05
S000001699	URA1		3449.57	1109.62	5.00E-05
S000004884	URA10		184.551	643.677	5.00E-05
S000003666	URA2		460.457	161.672	5.00E-05
S000000135	URA7		7.18839	23.0359	5.00E-05
S000003864	URA8		481.927	192.087	5.00E-05
S000004122	USB1		27.7841	11.892	5.00E-05
S000003645	UTP10		9.80806	32.0339	5.00E-05
S000004212	UTP13		8.40533	25.7264	5.00E-05
S000004558	UTP14		15.2124	45.8043	5.00E-05
S000004699	UTP15		22.1863	44.4245	5.00E-05
S000000100	UTP20		6.73298	15.7669	5.00E-05
S000004401	UTP21		6.9704	16.2939	5.00E-05
S000003322	UTP22		10.6215	21.9841	5.00E-05
S000001353	UTP25		15.7338	49.6615	5.00E-05
S000002732	UTP4		10.7259	31.9319	5.00E-05
S000002806	UTP5		20.0926	69.5283	5.00E-05
S000002857	UTP6		9.80822	30.8746	5.00E-05
S000003360	UTP8		8.0865	21.5078	5.00E-05
S000001239	UTP9		14.9338	45.3524	5.00E-05

S000004694	VBA1		34.3214	73.1853	5.00E-05
S000002655	VHS1		48.8163	118.071	5.00E-05
S000003297	VHT1		41.3829	16.3881	5.00E-05
S000004365	VID22		27.6128	9.74184	5.00E-05
S000001279	VID28		40.7551	18.0072	5.00E-05
S000000331	VMA2		220.166	501.788	5.00E-05
S000004409	VPS36		24.813	9.27581	5.00E-05
S000005886	VTS1		11.8472	34.4738	5.00E-05
S000113553	WIP1		243.754	121.186	5.00E-05
S000005227	WSC2		41.6844	17.5058	5.00E-05
S000001020	WSC4		10.9006	4.40312	5.00E-05
S000004060	XYL2		14.5293	45.4723	5.00E-05
S000007586	YAL044W-A		128.186	268.575	5.00E-05
S000003473	YAP1802		55.4476	23.5485	5.00E-05
S000002667	YAP6		27.762	92.4099	5.00E-05
S000005388	YAP7		44.0481	18.8251	5.00E-05
S000000089	YAR064W		4.69395	1.57743	0.02635
S000002146	YBL005W-A		7.55583	3.04152	0.0034
S000000106	YBL010C		22.0021	7.95807	5.00E-05
S000002149	YBL101W-B		3.5072	1.26537	5.00E-05
S000028736	YBR056W-A		147.285	36.4777	5.00E-05
S000000294	YBR090C		86.0611	203.791	0.00195
S000000342	YBR138C		24.3103	10.994	5.00E-05
S000000429	YBR225W		59.9754	28.4515	5.00E-05
S000029722	YBR230W-A		1161.23	489.779	5.00E-05
S000000442	YBR238C		4.17192	19.1429	5.00E-05
S000000488	YBR284W		43.3144	16.6762	5.00E-05
S000028605	YBR296C-A		112.793	0	0.00335
S000000524	YCL019W		7.72402	3.21023	5.00E-05
S000087203	YCL048W-A		209.201	552.821	5.00E-05
S000000639	YCR043C		82.0768	33.5152	5.00E-05
S000000699	YCR102C		6.19398	2.87467	0.00035
S000003978	YCT1		46.4696	441.383	5.00E-05
S000007588	YDL085C-A		137.359	45.2097	5.00E-05
S000007345	YDR034C-D		2.9432	1.03644	5.00E-05
S000007234	YDR034W-B		388.836	191.274	0.00275
S000002449	YDR042C		4.06537	1.71057	0.0059
S000002468	YDR061W		87.0635	185.931	5.00E-05
S000002541	YDR134C		793.331	4535.76	5.00E-05
S000028539	YDR182W-A		43.7707	8.96717	0.00285
S000007393	YDR210W-B		2.46705	0.977379	0.00015
S000002922	YDR514C		10.6869	34.9816	5.00E-05
S000000767	YEF1		29.8391	68.2886	5.00E-05
S000004239	YEF3		168.276	659.303	5.00E-05
S000000886	YER084W		131.79	34.6976	5.00E-05
S000000923	YER121W		50.543	108.341	5.00E-05
S000001903	YFH7		83.1418	171.449	5.00E-05
S000001830	YFL064C		5.85716	2.1875	0.0022
S000001828	YFL066C		14.8773	7.06997	5.00E-05
S000001827	YFL067W		83.0731	38.151	5.00E-05
S000002983	YGL015C		7.33835	1.62309	0.0024
S000003085	YGL117W		53.9536	146.559	5.00E-05
S000007607	YGL258W-A		37.8735	14.3774	0.0023
S000003231	YGL262W		11.6262	26.1135	5.00E-05
S000003249	YGR017W		94.2619	255.295	5.00E-05
S000007408	YGR038C-B		1.81285	0.517361	5.00E-05
S000003282	YGR050C		23.2148	11.43	0.0014
S000003311	YGR079W		22.4053	65.8213	5.00E-05
S000029726	YGR161W-C		398.57	1035.2	5.00E-05
S000003433	YGR201C		101.754	521.226	5.00E-05
S000003515	YGR283C		52.5266	25.3923	5.00E-05
S000003466	YHB1		87.6508	435.499	5.00E-05
S000001071	YHI9		16.8091	68.332	5.00E-05
S000001004	YHL012W		6.86755	15.2078	5.00E-05
S000001010	YHL018W		14.2089	5.02601	0.0004
S000001075	YHR033W		175.814	64.8394	5.00E-05

S000001169	YHR127W	15.3648	7.15079	0.0001
S000001182	YHR140W	62.8841	126.782	5.00E-05
S000001216	YHR173C	8.64805	3.67293	0.0137
S000028553	YHR175W-A	0	17.6371	0.00145
S000007421	YHR214C-C	31.3981	13.8187	5.00E-05
S000001268	YIA6	40.3498	10.8683	5.00E-05
S000005207	YIF1	77.1552	36.1537	5.00E-05
S000001339	YIL077C	213.689	549.625	5.00E-05
S000001364	YIL102C	7.13711	14.3815	0.01205
S000001370	YIL108W	92.6554	31.1503	5.00E-05
S000028838	YIR021W-A	3.34714	0	0.02285
S000003581	YJL045W	21.5268	60.2801	5.00E-05
S000003606	YJL070C	42.7596	17.2969	5.00E-05
S000003643	YJL107C	18.0504	3.56588	0.0001
S000003654	YJL118W	21.4693	7.12745	5.00E-05
S000003707	YJL171C	127.26	37.4334	5.00E-05
S000003717	YJL181W	8.16505	3.11234	5.00E-05
S000003754	YJL218W	2.73432	16.0186	5.00E-05
S000003791	YJR030C	20.0955	7.44727	5.00E-05
S000001527	YKL044W	106.541	52.3634	5.00E-05
S000113563	YKL065W-A	179.098	605.182	5.00E-05
S000028524	YKL068W-A	64.9466	188.309	5.00E-05
S000001554	YKL071W	22.4793	156.005	5.00E-05
S000001590	YKL107W	29.8427	64.9917	5.00E-05
S000001719	YKR011C	166.774	41.7582	5.00E-05
S000001783	YKR075C	701.703	1715.08	5.00E-05
S000003989	YLL066C	2.76219	1.31907	5.00E-05
S000004043	YLR053C	129.57	47.6765	5.00E-05
S000004115	YLR125W	26.1121	54.6177	5.00E-05
S000004142	YLR152C	59.9112	173.248	5.00E-05
S000004169	YLR179C	58.1411	176.298	5.00E-05
S000004215	YLR225C	136.4	28.9665	5.00E-05
S000007377	YLR256W-A	2.83988	0.954468	0.0001
S000004277	YLR287C	20.567	66.2958	5.00E-05
S000004288	YLR297W	104.413	260.385	5.00E-05
S000004438	YLR446W	114.282	52.7163	5.00E-05
S000004454	YLR462W	2.4882	0.70483	0.0109
S000000308	YMC2	13.1033	57.4381	5.00E-05
S000028688	YML100W-A	12.5406	0	0.00135
S000004689	YMR084W	29.9522	11.1552	5.00E-05
S000004690	YMR085W	48.6184	23.9853	5.00E-05
S000004696	YMR090W	459.853	935.655	5.00E-05
S000003871	YMR1	19.2515	7.55896	5.00E-05
S000004892	YMR279C	11.941	30.1839	5.00E-05
S000004932	YMR315W	80.0918	236.066	5.00E-05
S000004956	YNL011C	64.7333	32.042	5.00E-05
S000004963	YNL018C	13.9003	5.40541	5.00E-05
S000004964	YNL019C	8.55919	3.54371	0.0001
S000004979	YNL034W	10.5752	4.80866	5.00E-05
S000005090	YNL146W	23.0122	9.01471	0.0008
S000005139	YNL195C	160.338	455.189	5.00E-05
S000028852	YNL277W-A	28.7803	179.118	5.00E-05
S000005344	YNR061C	80.0503	32.3455	5.00E-05
S000005347	YNR064C	67.8714	20.7942	5.00E-05
S000005389	YOL029C	52.5713	24.1937	5.00E-05
S000007349	YOL103W-A	37.4605	14.6833	5.00E-05
S000005467	YOL107W	76.5035	18.8821	5.00E-05
S000005538	YOR012W	21.1637	46.8023	5.00E-05
S000028710	YOR032W-A	7.3547	34.6458	0.00645
S000005712	YOR186W	16.3442	88.3216	5.00E-05
S000005809	YOR283W	85.074	177.832	5.00E-05
S000005865	YOR338W	94.7629	676.218	5.00E-05
S000005869	YOR342C	32.4731	193.092	5.00E-05
S000007356	YOR343C-B	3.18579	1.1053	5.00E-05
S000005912	YOR385W	48.8264	17.4838	5.00E-05
S000005914	YOR387C	17.6529	40.7465	5.00E-05

S000005817	YPK9		29.6851	14.8284	5.00E-05
S000005935	YPL014W		20.9538	58.0988	5.00E-05
S000003430	YPP1		52.8972	301.726	5.00E-05
S000006331	YPR127W		145.454	388.119	5.00E-05
S000113589	YPR145C-A		12.5561	34.5897	0.0019
S000007361	YPR158C-C		37.6914	2.93501	0.02195
S000006400	YPR196W		27.8774	78.7152	5.00E-05
S000004110	YPS1		74.0056	25.6207	5.00E-05
S000003228	YPS5		28.4269	7.14941	5.00E-05
S000001147	YPT35		17.0654	42.6319	5.00E-05
S000002789	YRA1		827.07	77.764	5.00E-05
S000005688	YRR1		47.3375	164.659	5.00E-05
S000000315	YSA1		344.521	829.069	5.00E-05
S000002734	YSP2		23.042	10.2378	5.00E-05
S000000352	YSW1		5.59711	2.16076	5.00E-05
S000005798	YTM1		18.3404	60.9524	5.00E-05
S000003675	YUR1		25.3127	56.7502	5.00E-05
S000005613	YVC1		31.4238	12.1409	5.00E-05
S000001465	YVH1		9.78758	22.3789	5.00E-05
S000004577	ZDS2		9.40251	4.61172	5.00E-05
S000005469	ZEO1		4568.34	2058.71	5.00E-05

Table 4-A5. Full Gene Ontology terms based on up-regulated differentially expressed genes at 1 h in the S288c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
5975	carbohydrate metabolic process	1.24E-16	48	309	260	6440
16052	carbohydrate catabolic process	9.92E-16	27	309	86	6440
44262	cellular carbohydrate metabolic process	1.21E-15	36	309	158	6440
5984	disaccharide metabolic process	5.26E-10	13	309	31	6440
5991	trehalose metabolic process	3.74E-09	8	309	11	6440
9311	oligosaccharide metabolic process	4.74E-09	13	309	36	6440
44275	cellular carbohydrate catabolic process	4.79E-09	12	309	30	6440
70887	cellular response to chemical stimulus	5.62E-09	47	309	401	6440
42221	response to chemical	4.91E-08	58	309	588	6440
5992	trehalose biosynthetic process	7.82E-08	6	309	7	6440
9266	response to temperature stimulus	8.16E-08	19	309	95	6440
9628	response to abiotic stimulus	8.20E-08	29	309	202	6440
42026	protein refolding	1.50E-07	10	309	26	6440
55114	oxidation-reduction process	1.61E-07	47	309	446	6440
70413	trehalose metabolism in response to stress	2.47E-07	5	309	5	6440
46351	disaccharide biosynthetic process	3.00E-07	6	309	8	6440
6979	response to oxidative stress	3.36E-07	21	309	124	6440
9408	response to heat	9.39E-07	17	309	90	6440
34605	cellular response to heat	1.36E-06	15	309	73	6440
34599	cellular response to oxidative stress	1.39E-06	19	309	113	6440
9312	oligosaccharide biosynthetic process	2.07E-06	6	309	10	6440
51156	glucose 6-phosphate metabolic process	3.02E-06	8	309	21	6440
46365	monosaccharide catabolic process	7.02E-06	7	309	17	6440
46835	carbohydrate phosphorylation	7.02E-06	7	309	17	6440
44281	small molecule metabolic process	7.95E-06	64	309	782	6440
50896	response to stimulus	1.10E-05	93	309	1292	6440
1676	long-chain fatty acid metabolic process	1.22E-05	5	309	8	6440
6112	energy reserve metabolic process	1.26E-05	9	309	32	6440
272	polysaccharide catabolic process	1.67E-05	7	309	19	6440
6457	protein folding	1.75E-05	18	309	122	6440
72330	monocarboxylic acid biosynthetic process	1.88E-05	14	309	79	6440

6950	response to stress	3.16E-05	64	309	816	6440
9636	response to toxic substance	3.54E-05	13	309	73	6440
1901575	organic substance catabolic process	3.83E-05	57	309	704	6440
6458	de novo' protein folding	4.54E-05	9	309	37	6440
10035	response to inorganic substance	5.72E-05	12	309	66	6440
5976	polysaccharide metabolic process	5.76E-05	14	309	87	6440
5977	glycogen metabolic process	5.94E-05	8	309	30	6440
51085	chaperone cofactor-dependent protein refolding	6.19E-05	6	309	16	6440
42732	D-xylose metabolic process	7.22E-05	4	309	6	6440
6793	phosphorus metabolic process	7.27E-05	57	309	720	6440
46352	disaccharide catabolic process	9.18E-05	6	309	17	6440
51084	de novo' posttranslational protein folding	9.18E-05	6	309	17	6440
1905329	sphingoid long-chain base transport	1.09E-04	3	309	3	6440
35719	tRNA import into nucleus	1.09E-04	3	309	3	6440
5996	monosaccharide metabolic process	1.20E-04	12	309	71	6440
32787	monocarboxylic acid metabolic process	1.29E-04	21	309	180	6440
9313	oligosaccharide catabolic process	1.32E-04	6	309	18	6440
1904659	glucose transmembrane transport	1.56E-04	8	309	34	6440
8645	hexose transmembrane transport	1.56E-04	8	309	34	6440
15749	monosaccharide transmembrane transport	1.56E-04	8	309	34	6440
9414	response to water deprivation	1.62E-04	4	309	7	6440
42631	cellular response to water deprivation	1.62E-04	4	309	7	6440
44247	cellular polysaccharide catabolic process	1.62E-04	4	309	7	6440
34637	cellular carbohydrate biosynthetic process	1.70E-04	11	309	63	6440
44264	cellular polysaccharide metabolic process	1.81E-04	12	309	74	6440
6555	methionine metabolic process	1.92E-04	9	309	44	6440
34219	carbohydrate transmembrane transport	1.94E-04	8	309	35	6440
5978	glycogen biosynthetic process	2.30E-04	5	309	13	6440
51186	cofactor metabolic process	2.55E-04	26	309	259	6440
44272	sulfur compound biosynthetic process	2.66E-04	12	309	77	6440
8643	carbohydrate transport	2.74E-04	9	309	46	6440
6796	phosphate-containing compound metabolic process	2.75E-04	53	309	688	6440
6073	cellular glucan metabolic process	2.78E-04	10	309	56	6440
44042	glucan metabolic process	2.78E-04	10	309	56	6440
46496	nicotinamide nucleotide metabolic process	3.01E-04	12	309	78	6440

19362	pyridine nucleotide metabolic process	3.01E-04	12	309	78	6440
19323	pentose catabolic process	3.12E-04	4	309	8	6440
19388	galactose catabolic process	3.12E-04	4	309	8	6440
97237	cellular response to toxic substance	3.23E-04	10	309	57	6440
96	sulfur amino acid metabolic process	3.25E-04	9	309	47	6440
17144	drug metabolic process	4.13E-04	26	309	267	6440
101	sulfur amino acid transport	4.22E-04	3	309	4	6440
9269	response to desiccation	4.22E-04	3	309	4	6440
42759	long-chain fatty acid biosynthetic process	4.22E-04	3	309	4	6440
71465	cellular response to desiccation	4.22E-04	3	309	4	6440
42843	D-xylose catabolic process	4.22E-04	3	309	4	6440
5980	glycogen catabolic process	4.22E-04	3	309	4	6440
19413	acetate biosynthetic process	4.22E-04	3	309	4	6440
15750	pentose transmembrane transport	4.22E-04	3	309	4	6440
19751	polyol metabolic process	4.28E-04	7	309	30	6440
6739	NADP metabolic process	4.51E-04	6	309	22	6440
9056	catabolic process	5.12E-04	61	309	844	6440
9415	response to water	5.41E-04	4	309	9	6440
71462	cellular response to water stimulus	5.41E-04	4	309	9	6440
33554	cellular response to stress	5.72E-04	54	309	726	6440
1901700	response to oxygen-containing compound	6.05E-04	12	309	84	6440
44282	small molecule catabolic process	6.24E-04	17	309	147	6440
46394	carboxylic acid biosynthetic process	6.67E-04	22	309	217	6440
16053	organic acid biosynthetic process	6.67E-04	22	309	217	6440
6732	coenzyme metabolic process	6.79E-04	20	309	189	6440
19400	alditol metabolic process	6.94E-04	5	309	16	6440
35967	cellular response to topologically incorrect protein	7.40E-04	10	309	63	6440
51716	cellular response to stimulus	7.47E-04	74	309	1089	6440
46323	glucose import	7.94E-04	7	309	33	6440
16051	carbohydrate biosynthetic process	8.35E-04	12	309	87	6440
9251	glucan catabolic process	8.67E-04	4	309	10	6440
19320	hexose catabolic process	8.67E-04	4	309	10	6440
19321	pentose metabolic process	8.67E-04	4	309	10	6440
42908	xenobiotic transport	1.02E-03	3	309	5	6440
2001138	regulation of phospholipid transport	1.02E-03	3	309	5	6440

6404	RNA import into nucleus	1.02E-03	3	309	5	6440
19566	arabinose metabolic process	1.02E-03	3	309	5	6440
19568	arabinose catabolic process	1.02E-03	3	309	5	6440
61091	regulation of phospholipid translocation	1.02E-03	3	309	5	6440
6790	sulfur compound metabolic process	1.02E-03	16	309	140	6440
6066	alcohol metabolic process	1.03E-03	12	309	89	6440
72524	pyridine-containing compound metabolic process	1.13E-03	12	309	90	6440
15755	fructose transmembrane transport	1.26E-03	5	309	18	6440
6733	oxidoreduction coenzyme metabolic process	1.38E-03	12	309	92	6440
1901701	cellular response to oxygen-containing compound	1.41E-03	9	309	57	6440
302	response to reactive oxygen species	1.79E-03	6	309	28	6440
35966	response to topologically incorrect protein	1.90E-03	10	309	71	6440
19318	hexose metabolic process	2.04E-03	9	309	60	6440
6091	generation of precursor metabolites and energy	2.09E-03	20	309	207	6440
9086	methionine biosynthetic process	2.23E-03	7	309	39	6440
25	maltose catabolic process	2.30E-03	2	309	2	6440
34310	primary alcohol catabolic process	2.30E-03	2	309	2	6440
42883	cysteine transport	2.30E-03	2	309	2	6440
6059	hexitol metabolic process	2.30E-03	2	309	2	6440
6068	ethanol catabolic process	2.30E-03	2	309	2	6440
1903692	methionine import across plasma membrane	2.30E-03	2	309	2	6440
19588	anaerobic glycerol catabolic process	2.30E-03	2	309	2	6440
19594	mannitol metabolic process	2.30E-03	2	309	2	6440
19662	non-glycolytic fermentation	2.30E-03	2	309	2	6440
15821	methionine transport	2.30E-03	2	309	2	6440
23	maltose metabolic process	2.63E-03	4	309	13	6440
6012	galactose metabolic process	2.63E-03	4	309	13	6440
97035	regulation of membrane lipid distribution	2.65E-03	5	309	21	6440
19752	carboxylic acid metabolic process	2.75E-03	34	309	433	6440
97	sulfur amino acid biosynthetic process	3.01E-03	7	309	41	6440
42493	response to drug	3.14E-03	14	309	128	6440
9051	pentose-phosphate shunt, oxidative branch	3.31E-03	3	309	7	6440
33500	carbohydrate homeostasis	3.55E-03	4	309	14	6440
42542	response to hydrogen peroxide	3.55E-03	4	309	14	6440
42593	glucose homeostasis	3.55E-03	4	309	14	6440

1678	cellular glucose homeostasis	3.55E-03	4	309	14	6440
9117	nucleotide metabolic process	3.60E-03	21	309	232	6440
61077	chaperone-mediated protein folding	3.66E-03	6	309	32	6440
42737	drug catabolic process	3.97E-03	7	309	43	6440
6006	glucose metabolic process	3.97E-03	7	309	43	6440
19359	nicotinamide nucleotide biosynthetic process	3.97E-03	7	309	43	6440

Table 4-A6. Full Gene Ontology terms based on down-regulated differentially expressed genes at 1 h in the S288c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
42254	ribosome biogenesis	2.36E-42	98	286	477	6440
22613	ribonucleoprotein complex biogenesis	6.44E-36	99	286	572	6440
16072	rRNA metabolic process	4.62E-34	81	286	398	6440
34660	ncRNA metabolic process	4.43E-33	96	286	579	6440
6364	rRNA processing	1.27E-32	75	286	354	6440
34470	ncRNA processing	2.12E-32	86	286	473	6440
42273	ribosomal large subunit biogenesis	1.34E-25	41	286	125	6440
6396	RNA processing	3.24E-23	88	286	654	6440
42274	ribosomal small subunit biogenesis	1.15E-19	38	286	147	6440
462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.25E-18	32	286	108	6440
44085	cellular component biogenesis	2.07E-18	116	286	1213	6440
30490	maturation of SSU-rRNA	4.44E-18	33	286	120	6440
470	maturation of LSU-rRNA	1.11E-16	23	286	59	6440
463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.38E-16	20	286	45	6440
466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.71E-15	26	286	89	6440
460	maturation of 5.8S rRNA	5.02E-15	26	286	90	6440
16070	RNA metabolic process	1.20E-13	113	286	1341	6440
478	endonucleolytic cleavage involved in rRNA processing	3.11E-12	19	286	59	6440
479	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.11E-12	19	286	59	6440
1901360	organic cyclic compound metabolic process	5.19E-12	145	286	2035	6440
90304	nucleic acid metabolic process	3.67E-11	122	286	1626	6440
469	cleavage involved in rRNA processing	2.37E-10	20	286	82	6440
6725	cellular aromatic compound metabolic process	2.44E-10	137	286	1968	6440
46483	heterocycle metabolic process	3.32E-10	137	286	1976	6440
480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.14E-10	13	286	33	6440
6139	nucleobase-containing compound metabolic process	7.44E-10	131	286	1876	6440

967	rRNA 5'-end processing	2.72E-09	13	286	37	6440
447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.63E-09	14	286	46	6440
34471	ncRNA 5'-end processing	1.15E-08	13	286	41	6440
71840	cellular component organization or biogenesis	1.29E-08	149	286	2328	6440
472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.56E-08	12	286	35	6440
966	RNA 5'-end processing	1.60E-08	13	286	42	6440
10467	gene expression	3.74E-08	126	286	1883	6440
27	ribosomal large subunit assembly	2.08E-07	12	286	43	6440
90502	RNA phosphodiester bond hydrolysis, endonucleolytic	2.27E-07	22	286	142	6440
42255	ribosome assembly	3.71E-07	16	286	81	6440
34641	cellular nitrogen compound metabolic process	9.06E-07	155	286	2598	6440
90501	RNA phosphodiester bond hydrolysis	1.36E-06	25	286	195	6440
10501	RNA secondary structure unwinding	3.72E-06	9	286	30	6440
2181	cytoplasmic translation	8.93E-06	23	286	189	6440
90305	nucleic acid phosphodiester bond hydrolysis	5.95E-05	27	286	271	6440
42790	nucleolar large rRNA transcription by RNA polymerase I	5.95E-05	6	286	17	6440
71826	ribonucleoprotein complex subunit organization	7.93E-05	22	286	202	6440
464	endonucleolytic cleavage in ITS1 upstream of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	8.67E-05	3	286	3	6440
71428	rRNA-containing ribonucleoprotein complex export from nucleus	9.92E-05	11	286	64	6440
6360	transcription by RNA polymerase I	1.72E-04	8	286	37	6440
70925	organelle assembly	2.55E-04	19	286	175	6440
9303	rRNA transcription	2.67E-04	7	286	30	6440
22618	ribonucleoprotein complex assembly	2.67E-04	20	286	190	6440
6696	ergosterol biosynthetic process	4.97E-04	6	286	24	6440
44108	cellular alcohol biosynthetic process	4.97E-04	6	286	24	6440
97384	cellular lipid biosynthetic process	4.97E-04	6	286	24	6440
16129	phytosteroid biosynthetic process	4.97E-04	6	286	24	6440
98781	ncRNA transcription	5.41E-04	9	286	54	6440
71426	ribonucleoprotein complex export from nucleus	5.50E-04	15	286	129	6440

71166	ribonucleoprotein complex localization	5.97E-04	15	286	130	6440
16126	sterol biosynthetic process	6.05E-04	7	286	34	6440
1902653	secondary alcohol biosynthetic process	6.30E-04	6	286	25	6440
6611	protein export from nucleus	6.48E-04	15	286	131	6440
6405	RNA export from nucleus	7.02E-04	15	286	132	6440
6694	steroid biosynthetic process	7.28E-04	7	286	35	6440
51169	nuclear transport	7.62E-04	18	286	176	6440
6913	nucleocytoplasmic transport	7.62E-04	18	286	176	6440
16125	sterol metabolic process	8.20E-04	8	286	46	6440
51168	nuclear export	8.23E-04	15	286	134	6440
8202	steroid metabolic process	9.51E-04	8	286	47	6440
8204	ergosterol metabolic process	9.77E-04	6	286	27	6440
16128	phytosteroid metabolic process	9.77E-04	6	286	27	6440
1902652	secondary alcohol metabolic process	1.20E-03	6	286	28	6440
54	ribosomal subunit export from nucleus	1.26E-03	8	286	49	6440
44238	primary metabolic process	1.34E-03	189	286	3697	6440
33750	ribosome localization	1.45E-03	8	286	50	6440
1902299	pre-replicative complex assembly involved in cell cycle DNA replication	1.49E-03	5	286	20	6440
6267	pre-replicative complex assembly involved in nuclear cell cycle DNA replication	1.49E-03	5	286	20	6440
36388	pre-replicative complex assembly	1.49E-03	5	286	20	6440
44107	cellular alcohol metabolic process	1.75E-03	6	286	30	6440
2101	tRNA wobble cytosine modification	1.97E-03	2	286	2	6440
15827	tryptophan transport	1.97E-03	2	286	2	6440

Table 4-A7. Full Gene Ontology terms based on up-regulated differentially expressed genes at 4 h in the S288c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
5975	carbohydrate metabolic process	1.49E-11	52	477	260	6440
42026	protein refolding	3.23E-11	15	477	26	6440
44262	cellular carbohydrate metabolic process	1.44E-10	37	477	158	6440
9266	response to temperature stimulus	4.88E-10	27	477	95	6440
9408	response to heat	6.96E-10	26	477	90	6440
34605	cellular response to heat	1.03E-09	23	477	73	6440
5991	trehalose metabolic process	3.00E-09	9	477	11	6440
16052	carbohydrate catabolic process	6.87E-09	24	477	86	6440
5984	disaccharide metabolic process	1.02E-08	14	477	31	6440
6457	protein folding	1.05E-08	29	477	122	6440
6458	de novo' protein folding	1.82E-08	15	477	37	6440
70887	cellular response to chemical stimulus	2.55E-08	61	477	401	6440
9311	oligosaccharide metabolic process	1.03E-07	14	477	36	6440
42221	response to chemical	1.18E-07	78	477	588	6440
51085	chaperone cofactor-dependent protein refolding	4.46E-07	9	477	16	6440
9628	response to abiotic stimulus	5.07E-07	36	477	202	6440
51084	de novo' posttranslational protein folding	8.85E-07	9	477	17	6440
5992	trehalose biosynthetic process	1.05E-06	6	477	7	6440
70413	trehalose metabolism in response to stress	2.19E-06	5	477	5	6440
46351	disaccharide biosynthetic process	3.94E-06	6	477	8	6440
51156	glucose 6-phosphate metabolic process	8.18E-06	9	477	21	6440
6979	response to oxidative stress	1.00E-05	24	477	124	6440
61077	chaperone-mediated protein folding	1.01E-05	11	477	32	6440
1901575	organic substance catabolic process	1.23E-05	82	477	704	6440
34599	cellular response to oxidative stress	2.13E-05	22	477	113	6440
9312	oligosaccharide biosynthetic process	2.60E-05	6	477	10	6440
9056	catabolic process	2.87E-05	93	477	844	6440
44275	cellular carbohydrate catabolic process	3.51E-05	10	477	30	6440
35967	cellular response to topologically incorrect protein	3.92E-05	15	477	63	6440
35966	response to topologically incorrect protein	4.50E-05	16	477	71	6440
6112	energy reserve metabolic process	6.59E-05	10	477	32	6440

10035	response to inorganic substance	7.00E-05	15	477	66	6440
46365	monosaccharide catabolic process	1.18E-04	7	477	17	6440
46835	carbohydrate phosphorylation	1.18E-04	7	477	17	6440
5978	glycogen biosynthetic process	1.75E-04	6	477	13	6440
5977	glycogen metabolic process	2.18E-04	9	477	30	6440
42732	D-xylose metabolic process	3.95E-04	4	477	6	6440
43335	protein unfolding	4.04E-04	3	477	3	6440
35719	tRNA import into nucleus	4.04E-04	3	477	3	6440
44282	small molecule catabolic process	4.52E-04	23	477	147	6440
6950	response to stress	4.79E-04	85	477	816	6440
43618	regulation of transcription from RNA polymerase II promoter in response to stress	4.92E-04	13	477	62	6440
43620	regulation of DNA-templated transcription in response to stress	4.92E-04	13	477	62	6440
34620	cellular response to unfolded protein	5.05E-04	10	477	40	6440
5976	polysaccharide metabolic process	5.51E-04	16	477	87	6440
34637	cellular carbohydrate biosynthetic process	5.79E-04	13	477	63	6440
6986	response to unfolded protein	5.98E-04	11	477	48	6440
1901565	organonitrogen compound catabolic process	7.52E-04	48	477	408	6440
44248	cellular catabolic process	7.92E-04	81	477	782	6440
44281	small molecule metabolic process	7.92E-04	81	477	782	6440
7005	mitochondrion organization	8.24E-04	35	477	272	6440
9051	pentose-phosphate shunt, oxidative branch	8.69E-04	4	477	7	6440
9414	response to water deprivation	8.69E-04	4	477	7	6440
42631	cellular response to water deprivation	8.69E-04	4	477	7	6440
50896	response to stimulus	9.55E-04	123	477	1292	6440
46352	disaccharide catabolic process	9.78E-04	6	477	17	6440
71310	cellular response to organic substance	9.94E-04	27	477	194	6440
1901700	response to oxygen-containing compound	1.12E-03	15	477	84	6440

Table 4-A8. Full Gene Ontology terms based on down-regulated differentially expressed genes at 4 h in the S288c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
42254	ribosome biogenesis	2.36E-22	104	526	477	6440
16072	rRNA metabolic process	7.42E-20	89	526	398	6440
6364	rRNA processing	3.76E-18	80	526	354	6440
22613	ribonucleoprotein complex biogenesis	1.24E-17	107	526	572	6440
42274	ribosomal small subunit biogenesis	1.10E-15	45	526	147	6440
34660	ncRNA metabolic process	2.19E-15	103	526	579	6440
44085	cellular component biogenesis	3.14E-15	171	526	1213	6440
34470	ncRNA processing	8.17E-15	89	526	473	6440
42273	ribosomal large subunit biogenesis	4.84E-14	39	526	125	6440
30490	maturation of SSU-rRNA	6.07E-14	38	526	120	6440
6260	DNA replication	6.73E-14	40	526	132	6440
7049	cell cycle	6.91E-14	117	526	733	6440
462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2.86E-13	35	526	108	6440
22402	cell cycle process	1.06E-12	98	526	590	6440
6261	DNA-dependent DNA replication	1.34E-12	36	526	119	6440
1901360	organic cyclic compound metabolic process	3.64E-11	235	526	2035	6440
71840	cellular component organization or biogenesis	3.20E-10	257	526	2328	6440
470	maturation of LSU-rRNA	3.86E-10	22	526	59	6440
463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.08E-10	19	526	45	6440
466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	8.63E-10	27	526	89	6440
460	maturation of 5.8S rRNA	1.14E-09	27	526	90	6440
46483	heterocycle metabolic process	2.05E-09	223	526	1976	6440
7064	mitotic sister chromatid cohesion	2.33E-09	17	526	39	6440
6725	cellular aromatic compound metabolic process	2.42E-09	222	526	1968	6440
278	mitotic cell cycle	6.37E-09	60	526	343	6440
6396	RNA processing	1.15E-08	94	526	654	6440
6139	nucleobase-containing compound metabolic process	1.17E-08	211	526	1876	6440
478	endonucleolytic cleavage involved in rRNA processing	1.67E-08	20	526	59	6440

479	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.67E-08	20	526	59	6440
6302	double-strand break repair	4.50E-08	31	526	132	6440
1903047	mitotic cell cycle process	4.62E-08	56	526	327	6440
7062	sister chromatid cohesion	5.22E-08	19	526	57	6440
3	reproduction	6.59E-08	68	526	435	6440
90304	nucleic acid metabolic process	7.78E-08	185	526	1626	6440
22414	reproductive process	7.82E-08	66	526	419	6440
480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	9.48E-08	14	526	33	6440
447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.08E-07	16	526	46	6440
469	cleavage involved in rRNA processing	3.64E-07	22	526	82	6440
6281	DNA repair	4.42E-07	50	526	297	6440
51321	meiotic cell cycle	4.83E-07	52	526	315	6440
967	rRNA 5'-end processing	5.20E-07	14	526	37	6440
280	nuclear division	7.94E-07	37	526	195	6440
70	mitotic sister chromatid segregation	8.27E-07	24	526	99	6440
1903046	meiotic cell cycle process	9.05E-07	44	526	253	6440
6270	DNA replication initiation	1.10E-06	14	526	39	6440
33260	nuclear DNA replication	1.16E-06	13	526	34	6440
48285	organelle fission	1.17E-06	38	526	206	6440
51301	cell division	1.19E-06	49	526	298	6440
819	sister chromatid segregation	1.67E-06	27	526	124	6440
472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.71E-06	13	526	35	6440
44786	cell cycle DNA replication	1.71E-06	13	526	35	6440
6974	cellular response to DNA damage stimulus	1.95E-06	54	526	347	6440
34471	ncRNA 5'-end processing	2.21E-06	14	526	41	6440
6271	DNA strand elongation involved in DNA replication	2.48E-06	13	526	36	6440
140014	mitotic nuclear division	2.52E-06	25	526	112	6440
966	RNA 5'-end processing	3.07E-06	14	526	42	6440
19752	carboxylic acid metabolic process	5.73E-06	62	526	433	6440
98813	nuclear chromosome segregation	5.90E-06	30	526	155	6440

98656	anion transmembrane transport	6.43E-06	22	526	96	6440
10927	cellular component assembly involved in morphogenesis	6.55E-06	18	526	69	6440
6273	lagging strand elongation	6.64E-06	9	526	19	6440
19953	sexual reproduction	6.92E-06	32	526	172	6440
44703	multi-organism reproductive process	6.92E-06	32	526	172	6440
22616	DNA strand elongation	6.94E-06	13	526	39	6440
724	double-strand break repair via homologous recombination	7.18E-06	19	526	76	6440
32989	cellular component morphogenesis	7.72E-06	21	526	90	6440
44281	small molecule metabolic process	8.18E-06	97	526	782	6440
43436	oxoacid metabolic process	1.09E-05	63	526	451	6440
731	DNA synthesis involved in DNA repair	1.12E-05	9	526	20	6440
6082	organic acid metabolic process	1.26E-05	63	526	453	6440
7059	chromosome segregation	1.79E-05	33	526	188	6440
32787	monocarboxylic acid metabolic process	1.83E-05	32	526	180	6440
1902969	mitotic DNA replication	1.96E-05	6	526	9	6440
1903825	organic acid transmembrane transport	1.98E-05	16	526	61	6440
46459	short-chain fatty acid metabolic process	2.00E-05	5	526	6	6440
72350	tricarboxylic acid metabolic process	2.57E-05	11	526	32	6440
70925	organelle assembly	2.67E-05	31	526	175	6440
725	recombinational repair	2.79E-05	19	526	83	6440
31505	fungal-type cell wall organization	2.80E-05	33	526	192	6440
51704	multi-organism process	3.12E-05	33	526	193	6440
32505	reproduction of a single-celled organism	3.12E-05	33	526	193	6440
19541	propionate metabolic process	4.40E-05	4	526	4	6440
1901615	organic hydroxy compound metabolic process	5.17E-05	25	526	132	6440
1905039	carboxylic acid transmembrane transport	5.35E-05	15	526	59	6440
71852	fungal-type cell wall organization or biogenesis	6.55E-05	36	526	226	6440
42255	ribosome assembly	6.87E-05	18	526	81	6440
1901617	organic hydroxy compound biosynthetic process	8.37E-05	17	526	75	6440
45229	external encapsulating structure organization	8.80E-05	37	526	238	6440
71555	cell wall organization	8.80E-05	37	526	238	6440
7076	mitotic chromosome condensation	9.34E-05	6	526	11	6440
45005	DNA-dependent DNA replication maintenance of fidelity	9.39E-05	9	526	25	6440
1902299	pre-replicative complex assembly involved in cell cycle DNA replication	9.78E-05	8	526	20	6440

	pre-replicative complex assembly involved in nuclear cell cycle					
6267	DNA replication	9.78E-05	8	526	20	6440
36388	pre-replicative complex assembly	9.78E-05	8	526	20	6440
6099	tricarboxylic acid cycle	1.11E-04	10	526	31	6440
6101	citrate metabolic process	1.11E-04	10	526	31	6440
27	ribosomal large subunit assembly	1.13E-04	12	526	43	6440
43570	maintenance of DNA repeat elements	1.33E-04	9	526	26	6440
45143	homologous chromosome segregation	1.52E-04	11	526	38	6440
44283	small molecule biosynthetic process	1.60E-04	49	526	356	6440
6188	IMP biosynthetic process	1.74E-04	6	526	12	6440
61982	meiosis I cell cycle process	1.76E-04	20	526	102	6440
71709	membrane assembly	2.19E-04	7	526	17	6440
44091	membrane biogenesis	2.19E-04	7	526	17	6440
32120	ascospore-type prospore membrane assembly	2.19E-04	7	526	17	6440
22413	reproductive process in single-celled organism	2.22E-04	25	526	144	6440
16070	RNA metabolic process	2.43E-04	142	526	1341	6440
9653	anatomical structure morphogenesis	2.88E-04	31	526	198	6440
6259	DNA metabolic process	2.98E-04	63	526	503	6440
46040	IMP metabolic process	3.01E-04	6	526	13	6440
31321	ascospore-type prospore assembly	3.06E-04	8	526	23	6440
3006	developmental process involved in reproduction	3.27E-04	26	526	156	6440
19985	translesion synthesis	3.34E-04	7	526	18	6440
6075	(1->3)-beta-D-glucan biosynthetic process	3.41E-04	5	526	9	6440
6189	de novo' IMP biosynthetic process	3.41E-04	5	526	9	6440
6301	postreplication repair	3.42E-04	9	526	29	6440
30437	ascospore formation	3.45E-04	21	526	115	6440
7127	meiosis I	3.79E-04	18	526	92	6440
48468	cell development	3.89E-04	21	526	116	6440
42723	thiamine-containing compound metabolic process	4.90E-04	6	526	14	6440
921	septin ring assembly	4.92E-04	7	526	19	6440
464	endonucleolytic cleavage in ITS1 upstream of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.42E-04	3	526	3	6440
1902292	cell cycle DNA replication initiation	5.42E-04	3	526	3	6440
1902315	nuclear cell cycle DNA replication initiation	5.42E-04	3	526	3	6440

1902975	mitotic DNA replication initiation	5.42E-04	3	526	3	6440
19543	propionate catabolic process	5.42E-04	3	526	3	6440
19626	short-chain fatty acid catabolic process	5.42E-04	3	526	3	6440
19629	propionate catabolic process, 2-methylcitrate cycle	5.42E-04	3	526	3	6440
34293	sexual sporulation	5.56E-04	21	526	119	6440
43935	sexual sporulation resulting in formation of a cellular spore	5.56E-04	21	526	119	6440
43111	replication fork arrest	5.78E-04	4	526	6	6440
48856	anatomical structure development	5.83E-04	31	526	206	6440
71554	cell wall organization or biogenesis	6.17E-04	40	526	290	6440
6090	pyruvate metabolic process	6.19E-04	11	526	44	6440
140013	meiotic nuclear division	6.39E-04	20	526	112	6440
32185	septin cytoskeleton organization	7.04E-04	10	526	38	6440
6094	gluconeogenesis	7.04E-04	7	526	20	6440
19319	hexose biosynthetic process	7.04E-04	7	526	20	6440
48646	anatomical structure formation involved in morphogenesis	7.38E-04	27	526	173	6440
34087	establishment of mitotic sister chromatid cohesion	7.62E-04	6	526	15	6440
727	double-strand break repair via break-induced replication	7.82E-04	8	526	26	6440
15849	organic acid transport	8.36E-04	18	526	98	6440
16125	sterol metabolic process	9.27E-04	11	526	46	6440
46165	alcohol biosynthetic process	9.27E-04	12	526	53	6440
6275	regulation of DNA replication	9.27E-04	12	526	53	6440
51274	beta-glucan biosynthetic process	9.83E-04	7	526	21	6440
90502	RNA phosphodiester bond hydrolysis, endonucleolytic	1.07E-03	23	526	142	6440
6074	(1->3)-beta-D-glucan metabolic process	1.09E-03	5	526	11	6440
1902808	positive regulation of cell cycle G1/S phase transition	1.09E-03	5	526	11	6440
1900087	positive regulation of G1/S transition of mitotic cell cycle	1.09E-03	5	526	11	6440
3333	amino acid transmembrane transport	1.09E-03	10	526	40	6440
8202	steroid metabolic process	1.12E-03	11	526	47	6440
71897	DNA biosynthetic process	1.20E-03	18	526	101	6440
31106	septin ring organization	1.24E-03	9	526	34	6440
16126	sterol biosynthetic process	1.24E-03	9	526	34	6440
51276	chromosome organization	1.24E-03	67	526	572	6440
71103	DNA conformation change	1.26E-03	20	526	118	6440
70058	tRNA gene clustering	1.26E-03	4	526	7	6440
30466	chromatin silencing at silent mating-type cassette	1.34E-03	10	526	41	6440

46364	monosaccharide biosynthetic process	1.34E-03	7	526	22	6440
6694	steroid biosynthetic process	1.55E-03	9	526	35	6440
9272	fungal-type cell wall biogenesis	1.58E-03	16	526	87	6440
16051	carbohydrate biosynthetic process	1.58E-03	16	526	87	6440
34085	establishment of sister chromatid cohesion	1.63E-03	6	526	17	6440
42790	nucleolar large rRNA transcription by RNA polymerase I	1.63E-03	6	526	17	6440
33567	DNA replication, Okazaki fragment processing	1.74E-03	5	526	12	6440
9228	thiamine biosynthetic process	1.74E-03	5	526	12	6440
9262	deoxyribonucleotide metabolic process	1.74E-03	5	526	12	6440
9263	deoxyribonucleotide biosynthetic process	1.74E-03	5	526	12	6440
2000104	negative regulation of DNA-dependent DNA replication	1.74E-03	5	526	12	6440
70987	error-free translesion synthesis	1.74E-03	5	526	12	6440
42724	thiamine-containing compound biosynthetic process	1.74E-03	5	526	12	6440
46942	carboxylic acid transport	1.76E-03	17	526	96	6440
51273	beta-glucan metabolic process	1.79E-03	7	526	23	6440
70591	ascospore wall biogenesis	1.92E-03	11	526	50	6440
70590	spore wall biogenesis	1.92E-03	11	526	50	6440
42244	spore wall assembly	1.92E-03	11	526	50	6440
30476	ascospore wall assembly	1.92E-03	11	526	50	6440
45132	meiotic chromosome segregation	1.95E-03	13	526	65	6440
35524	proline transmembrane transport	2.04E-03	3	526	4	6440
44879	morphogenesis checkpoint	2.04E-03	3	526	4	6440
9303	rRNA transcription	2.19E-03	8	526	30	6440
71940	fungal-type cell wall assembly	2.28E-03	11	526	51	6440
30261	chromosome condensation	2.29E-03	6	526	18	6440
6541	glutamine metabolic process	2.36E-03	7	526	24	6440
6696	ergosterol biosynthetic process	2.36E-03	7	526	24	6440
7129	synapsis	2.36E-03	7	526	24	6440
44108	cellular alcohol biosynthetic process	2.36E-03	7	526	24	6440
97384	cellular lipid biosynthetic process	2.36E-03	7	526	24	6440
15718	monocarboxylic acid transport	2.36E-03	7	526	24	6440
16129	phytosteroid biosynthetic process	2.36E-03	7	526	24	6440
70192	chromosome organization involved in meiotic cell cycle	2.37E-03	10	526	44	6440
72527	pyrimidine-containing compound metabolic process	2.37E-03	10	526	44	6440
34641	cellular nitrogen compound metabolic process	2.59E-03	243	526	2598	6440

6772	thiamine metabolic process	2.64E-03	5	526	13	6440
70726	cell wall assembly	2.68E-03	11	526	52	6440
30435	sporulation resulting in formation of a cellular spore	2.90E-03	25	526	171	6440
1901992	positive regulation of mitotic cell cycle phase transition	3.05E-03	7	526	25	6440
1902653	secondary alcohol biosynthetic process	3.05E-03	7	526	25	6440
6284	base-excision repair	3.11E-03	6	526	19	6440
43934	sporulation	3.14E-03	25	526	172	6440
16458	gene silencing	3.17E-03	21	526	136	6440
17144	drug metabolic process	3.21E-03	35	526	267	6440
98781	ncRNA transcription	3.66E-03	11	526	54	6440
747	conjugation with cellular fusion	3.66E-03	11	526	54	6440
45814	negative regulation of gene expression, epigenetic	3.75E-03	20	526	129	6440
6342	chromatin silencing	3.75E-03	20	526	129	6440
44764	multi-organism cellular process	3.82E-03	12	526	62	6440
1901989	positive regulation of cell cycle phase transition	3.88E-03	7	526	26	6440
710	meiotic mismatch repair	3.98E-03	4	526	9	6440
72528	pyrimidine-containing compound biosynthetic process	4.16E-03	9	526	40	6440
9250	glucan biosynthetic process	4.18E-03	8	526	33	6440
51052	regulation of DNA metabolic process	4.35E-03	18	526	113	6440
90501	RNA phosphodiester bond hydrolysis	4.37E-03	27	526	195	6440
6348	chromatin silencing at telomere	4.38E-03	12	526	63	6440
1901293	nucleoside phosphate biosynthetic process	4.50E-03	21	526	140	6440
1990683	DNA double-strand break attachment to nuclear envelope	4.78E-03	3	526	5	6440
34407	cell wall (1->3)-beta-D-glucan metabolic process	4.78E-03	3	526	5	6440
34410	cell wall beta-glucan biosynthetic process	4.78E-03	3	526	5	6440
34411	cell wall (1->3)-beta-D-glucan biosynthetic process	4.78E-03	3	526	5	6440
34723	DNA replication-dependent nucleosome organization	4.78E-03	3	526	5	6440
6335	DNA replication-dependent nucleosome assembly	4.78E-03	3	526	5	6440
71969	fungal-type cell wall (1->3)-beta-D-glucan metabolic process	4.78E-03	3	526	5	6440
71970	fungal-type cell wall (1->3)-beta-D-glucan biosynthetic process	4.78E-03	3	526	5	6440
42546	cell wall biogenesis	4.78E-03	18	526	114	6440
8204	ergosterol metabolic process	4.88E-03	7	526	27	6440
16128	phytosteroid metabolic process	4.88E-03	7	526	27	6440
746	conjugation	4.91E-03	11	526	56	6440

Table 4-A9. Full Gene Ontology terms based on up-regulated differentially expressed genes at 4 h in the S7 strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
5975	carbohydrate metabolic process	6.94E-16	37	194	260	6440
16052	carbohydrate catabolic process	4.81E-11	18	194	86	6440
6006	glucose metabolic process	1.86E-10	13	194	43	6440
19318	hexose metabolic process	1.63E-09	14	194	60	6440
9311	oligosaccharide metabolic process	4.35E-09	11	194	36	6440
16051	carbohydrate biosynthetic process	4.49E-09	16	194	87	6440
5992	trehalose biosynthetic process	4.73E-09	6	194	7	6440
46496	nicotinamide nucleotide metabolic process	7.33E-09	15	194	78	6440
19362	pyridine nucleotide metabolic process	7.33E-09	15	194	78	6440
44262	cellular carbohydrate metabolic process	7.64E-09	21	194	158	6440
6733	oxidoreduction coenzyme metabolic process	1.05E-08	16	194	92	6440
5984	disaccharide metabolic process	1.25E-08	10	194	31	6440
5996	monosaccharide metabolic process	1.69E-08	14	194	71	6440
46351	disaccharide biosynthetic process	1.84E-08	6	194	8	6440
46031	ADP metabolic process	2.47E-08	10	194	33	6440
9135	purine nucleoside diphosphate metabolic process	3.41E-08	10	194	34	6440
9179	purine ribonucleoside diphosphate metabolic process	3.41E-08	10	194	34	6440
9185	ribonucleoside diphosphate metabolic process	3.41E-08	10	194	34	6440
6090	pyruvate metabolic process	4.49E-08	11	194	44	6440
72524	pyridine-containing compound metabolic process	5.59E-08	15	194	90	6440
9132	nucleoside diphosphate metabolic process	8.38E-08	10	194	37	6440
278	mitotic cell cycle	9.21E-08	30	194	343	6440
1903047	mitotic cell cycle process	1.15E-07	29	194	327	6440
9312	oligosaccharide biosynthetic process	1.31E-07	6	194	10	6440
44281	small molecule metabolic process	2.63E-07	49	194	782	6440
5991	trehalose metabolic process	2.82E-07	6	194	11	6440
42866	pyruvate biosynthetic process	5.76E-07	8	194	26	6440
6096	glycolytic process	5.76E-07	8	194	26	6440
6757	ATP generation from ADP	5.76E-07	8	194	26	6440
44283	small molecule biosynthetic process	7.04E-07	29	194	356	6440

6165	nucleoside diphosphate phosphorylation	1.09E-06	8	194	28	6440
6094	gluconeogenesis	1.12E-06	7	194	20	6440
19319	hexose biosynthetic process	1.12E-06	7	194	20	6440
46434	organophosphate catabolic process	1.18E-06	10	194	48	6440
32787	monocarboxylic acid metabolic process	1.62E-06	19	194	180	6440
6066	alcohol metabolic process	2.12E-06	13	194	89	6440
46364	monosaccharide biosynthetic process	2.35E-06	7	194	22	6440
51186	cofactor metabolic process	2.61E-06	23	194	259	6440
9166	nucleotide catabolic process	3.32E-06	8	194	32	6440
6732	coenzyme metabolic process	3.37E-06	19	194	189	6440
72330	monocarboxylic acid biosynthetic process	3.47E-06	12	194	79	6440
1901292	nucleoside phosphate catabolic process	4.27E-06	8	194	33	6440
46323	glucose import	4.27E-06	8	194	33	6440
1904659	glucose transmembrane transport	5.44E-06	8	194	34	6440
8645	hexose transmembrane transport	5.44E-06	8	194	34	6440
15749	monosaccharide transmembrane transport	5.44E-06	8	194	34	6440
34219	carbohydrate transmembrane transport	6.87E-06	8	194	35	6440
46939	nucleotide phosphorylation	6.87E-06	8	194	35	6440
8643	carbohydrate transport	7.12E-06	9	194	46	6440
51301	cell division	8.62E-06	24	194	298	6440
15755	fructose transmembrane transport	9.49E-06	6	194	18	6440
22402	cell cycle process	1.07E-05	37	194	590	6440
44275	cellular carbohydrate catabolic process	2.28E-05	7	194	30	6440
34404	nucleobase-containing small molecule biosynthetic process	2.37E-05	10	194	66	6440
9145	purine nucleoside triphosphate biosynthetic process	2.39E-05	9	194	53	6440
9206	purine ribonucleoside triphosphate biosynthetic process	2.39E-05	9	194	53	6440
51156	glucose 6-phosphate metabolic process	2.57E-05	6	194	21	6440
19359	nicotinamide nucleotide biosynthetic process	3.44E-05	8	194	43	6440
1901615	organic hydroxy compound metabolic process	3.82E-05	14	194	132	6440
19363	pyridine nucleotide biosynthetic process	4.10E-05	8	194	44	6440
9201	ribonucleoside triphosphate biosynthetic process	4.37E-05	9	194	57	6440
17144	drug metabolic process	4.67E-05	21	194	267	6440
5976	polysaccharide metabolic process	5.29E-05	11	194	87	6440
6696	ergosterol biosynthetic process	5.92E-05	6	194	24	6440
44108	cellular alcohol biosynthetic process	5.92E-05	6	194	24	6440

97384	cellular lipid biosynthetic process	5.92E-05	6	194	24	6440
16129	phytosteroid biosynthetic process	5.92E-05	6	194	24	6440
55086	nucleobase-containing small molecule metabolic process	6.46E-05	21	194	273	6440
44264	cellular polysaccharide metabolic process	6.54E-05	10	194	74	6440
43436	oxoacid metabolic process	7.13E-05	29	194	451	6440
9142	nucleoside triphosphate biosynthetic process	7.58E-05	9	194	61	6440
1902653	secondary alcohol biosynthetic process	7.59E-05	6	194	25	6440
6082	organic acid metabolic process	7.72E-05	29	194	453	6440
15761	mannose transmembrane transport	7.85E-05	5	194	16	6440
6754	ATP biosynthetic process	7.87E-05	8	194	48	6440
19752	carboxylic acid metabolic process	8.73E-05	28	194	433	6440
34637	cellular carbohydrate biosynthetic process	9.83E-05	9	194	63	6440
1901135	carbohydrate derivative metabolic process	1.18E-04	25	194	372	6440
910	cytokinesis	1.19E-04	11	194	95	6440
8204	ergosterol metabolic process	1.21E-04	6	194	27	6440
16128	phytosteroid metabolic process	1.21E-04	6	194	27	6440
44282	small molecule catabolic process	1.25E-04	14	194	147	6440
19693	ribose phosphate metabolic process	1.49E-04	15	194	168	6440
1902652	secondary alcohol metabolic process	1.50E-04	6	194	28	6440
61640	cytoskeleton-dependent cytokinesis	1.58E-04	10	194	82	6440
6928	movement of cell or subcellular component	1.62E-04	7	194	40	6440
46165	alcohol biosynthetic process	1.62E-04	8	194	53	6440
9117	nucleotide metabolic process	1.98E-04	18	194	232	6440
9205	purine ribonucleoside triphosphate metabolic process	2.08E-04	11	194	101	6440
44107	cellular alcohol metabolic process	2.24E-04	6	194	30	6440
9127	purine nucleoside monophosphate biosynthetic process	2.25E-04	9	194	70	6440
9168	purine ribonucleoside monophosphate biosynthetic process	2.25E-04	9	194	70	6440
7049	cell cycle	2.40E-04	39	194	733	6440
72525	pyridine-containing compound biosynthetic process	2.41E-04	8	194	56	6440
9144	purine nucleoside triphosphate metabolic process	2.47E-04	11	194	103	6440
70413	trehalose metabolism in response to stress	2.57E-04	3	194	5	6440
6011	UDP-glucose metabolic process	2.57E-04	3	194	5	6440
6753	nucleoside phosphate metabolic process	2.58E-04	18	194	237	6440
46394	carboxylic acid biosynthetic process	2.67E-04	17	194	217	6440
16053	organic acid biosynthetic process	2.67E-04	17	194	217	6440

9156	ribonucleoside monophosphate biosynthetic process	2.85E-04	10	194	88	6440
9199	ribonucleoside triphosphate metabolic process	2.93E-04	11	194	105	6440
16125	sterol metabolic process	3.99E-04	7	194	46	6440
6739	NADP metabolic process	4.08E-04	5	194	22	6440
281	mitotic cytokinesis	4.22E-04	9	194	76	6440
9124	nucleoside monophosphate biosynthetic process	4.48E-04	10	194	93	6440
1901575	organic substance catabolic process	4.56E-04	37	194	704	6440
8202	steroid metabolic process	4.57E-04	7	194	47	6440
16126	sterol biosynthetic process	4.60E-04	6	194	34	6440
6012	galactose metabolic process	4.61E-04	4	194	13	6440
6091	generation of precursor metabolites and energy	4.71E-04	16	194	207	6440
10638	positive regulation of organelle organization	4.76E-04	11	194	111	6440
9259	ribonucleotide metabolic process	4.84E-04	13	194	148	6440
15757	galactose transmembrane transport	5.03E-04	3	194	6	6440
1902850	microtubule cytoskeleton organization involved in mitosis	5.22E-04	7	194	48	6440
9260	ribonucleotide biosynthetic process	5.32E-04	10	194	95	6440
6694	steroid biosynthetic process	5.41E-04	6	194	35	6440
7052	mitotic spindle organization	5.41E-04	6	194	35	6440
46034	ATP metabolic process	5.78E-04	10	194	96	6440
9141	nucleoside triphosphate metabolic process	5.98E-04	11	194	114	6440
9152	purine ribonucleotide biosynthetic process	6.19E-04	9	194	80	6440
9150	purine ribonucleotide metabolic process	6.26E-04	12	194	133	6440
6793	phosphorus metabolic process	7.03E-04	37	194	720	6440
55114	oxidation-reduction process	8.04E-04	26	194	446	6440
6164	purine nucleotide biosynthetic process	8.12E-04	9	194	83	6440
6163	purine nucleotide metabolic process	8.17E-04	12	194	137	6440
19682	glyceraldehyde-3-phosphate metabolic process	8.40E-04	4	194	15	6440
2000601	positive regulation of Arp2/3 complex-mediated actin nucleation	8.62E-04	3	194	7	6440
51127	positive regulation of actin nucleation	8.62E-04	3	194	7	6440
44247	cellular polysaccharide catabolic process	8.62E-04	3	194	7	6440
46390	ribose phosphate biosynthetic process	8.65E-04	10	194	101	6440
9161	ribonucleoside monophosphate metabolic process	8.71E-04	12	194	138	6440
6059	hexitol metabolic process	9.03E-04	2	194	2	6440
6527	arginine catabolic process	9.03E-04	2	194	2	6440
51645	Golgi localization	9.03E-04	2	194	2	6440

19255	glucose 1-phosphate metabolic process	9.03E-04	2	194	2	6440
19594	mannitol metabolic process	9.03E-04	2	194	2	6440
9126	purine nucleoside monophosphate metabolic process	9.22E-04	11	194	120	6440
9167	purine ribonucleoside monophosphate metabolic process	9.22E-04	11	194	120	6440
44770	cell cycle phase transition	1.05E-03	9	194	86	6440
44772	mitotic cell cycle phase transition	1.05E-03	9	194	86	6440
6067	ethanol metabolic process	1.09E-03	4	194	16	6440
9123	nucleoside monophosphate metabolic process	1.19E-03	12	194	143	6440
6073	cellular glucan metabolic process	1.34E-03	7	194	56	6440
44042	glucan metabolic process	1.34E-03	7	194	56	6440
19388	galactose catabolic process	1.35E-03	3	194	8	6440
46352	disaccharide catabolic process	1.40E-03	4	194	17	6440
34308	primary alcohol metabolic process	1.40E-03	4	194	17	6440
72522	purine-containing compound biosynthetic process	1.57E-03	9	194	91	6440
7051	spindle organization	1.66E-03	6	194	43	6440
51493	regulation of cytoskeleton organization	1.70E-03	9	194	92	6440
9313	oligosaccharide catabolic process	1.75E-03	4	194	18	6440
1901617	organic hydroxy compound biosynthetic process	1.76E-03	8	194	75	6440
9108	coenzyme biosynthetic process	1.78E-03	11	194	130	6440
5977	glycogen metabolic process	1.82E-03	5	194	30	6440
7018	microtubule-based movement	1.82E-03	5	194	30	6440
60236	regulation of mitotic spindle organization	1.98E-03	3	194	9	6440
272	polysaccharide catabolic process	2.17E-03	4	194	19	6440
82	G1/S transition of mitotic cell cycle	2.22E-03	7	194	61	6440
44843	cell cycle G1/S phase transition	2.22E-03	7	194	61	6440
6796	phosphate-containing compound metabolic process	2.33E-03	34	194	688	6440
72521	purine-containing compound metabolic process	2.38E-03	12	194	155	6440
70507	regulation of microtubule cytoskeleton organization	2.45E-03	5	194	32	6440
6112	energy reserve metabolic process	2.45E-03	5	194	32	6440
44571	[2Fe-2S] cluster assembly	2.65E-03	2	194	3	6440
90224	regulation of spindle organization	2.76E-03	3	194	10	6440
19320	hexose catabolic process	2.76E-03	3	194	10	6440
32886	regulation of microtubule-based process	2.81E-03	5	194	33	6440
19637	organophosphate metabolic process	3.14E-03	23	194	415	6440
30866	cortical actin cytoskeleton organization	3.22E-03	5	194	34	6440

2001252	positive regulation of chromosome organization	3.22E-03	5	194	34	6440
9056	catabolic process	3.64E-03	39	194	844	6440
30865	cortical cytoskeleton organization	3.67E-03	5	194	35	6440
33692	cellular polysaccharide biosynthetic process	4.44E-03	6	194	52	6440
7010	cytoskeleton organization	4.49E-03	15	194	234	6440
51302	regulation of cell division	4.51E-03	4	194	23	6440
15696	ammonium transport	4.51E-03	4	194	23	6440
50667	homocysteine metabolic process	4.84E-03	3	194	12	6440
34315	regulation of Arp2/3 complex-mediated actin nucleation	4.84E-03	3	194	12	6440
51125	regulation of actin nucleation	4.84E-03	3	194	12	6440
271	polysaccharide biosynthetic process	4.89E-03	6	194	53	6440
31505	fungal-type cell wall organization	5.09E-03	13	194	192	6440
1904668	positive regulation of ubiquitin protein ligase activity	5.20E-03	2	194	4	6440
1904666	regulation of ubiquitin protein ligase activity	5.20E-03	2	194	4	6440
916	actomyosin contractile ring contraction	5.20E-03	2	194	4	6440
2000574	regulation of microtubule motor activity	5.20E-03	2	194	4	6440
48313	Golgi inheritance	5.20E-03	2	194	4	6440
36213	contractile ring contraction	5.20E-03	2	194	4	6440
15750	pentose transmembrane transport	5.20E-03	2	194	4	6440
1900049	regulation of histone exchange	5.20E-03	2	194	4	6440
51495	positive regulation of cytoskeleton organization	5.36E-03	6	194	54	6440
280	nuclear division	5.79E-03	13	194	195	6440
51130	positive regulation of cellular component organization	5.96E-03	11	194	152	6440
15672	monovalent inorganic cation transport	6.06E-03	9	194	111	6440
22	mitotic spindle elongation	6.16E-03	3	194	13	6440
23	maltose metabolic process	6.16E-03	3	194	13	6440
5978	glycogen biosynthetic process	6.16E-03	3	194	13	6440
51231	spindle elongation	6.16E-03	3	194	13	6440

Table 4-A10. Full Gene Ontology terms based on down-regulated differentially expressed genes at 4 h in the S7 strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
42254	ribosome biogenesis	4.26E-102	169	364	477	6440
22613	ribonucleoprotein complex biogenesis	1.46E-89	171	364	572	6440
16072	rRNA metabolic process	4.32E-85	143	364	398	6440
6364	rRNA processing	1.01E-83	135	364	354	6440
34660	ncRNA metabolic process	4.67E-80	163	364	579	6440
34470	ncRNA processing	1.20E-78	148	364	473	6440
6396	RNA processing	4.03E-59	150	364	654	6440
42274	ribosomal small subunit biogenesis	3.99E-52	72	364	147	6440
462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.32E-47	60	364	108	6440
30490	maturation of SSU-rRNA	1.32E-46	62	364	120	6440
44085	cellular component biogenesis	6.11E-44	182	364	1213	6440
42273	ribosomal large subunit biogenesis	3.85E-40	58	364	125	6440
460	maturation of 5.8S rRNA	6.26E-37	48	364	90	6440
466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	6.69E-36	47	364	89	6440
16070	RNA metabolic process	4.33E-33	175	364	1341	6440
447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	8.44E-32	33	364	46	6440
478	endonucleolytic cleavage involved in rRNA processing	9.83E-31	36	364	59	6440
479	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	9.83E-31	36	364	59	6440
469	cleavage involved in rRNA processing	4.03E-30	41	364	82	6440
967	rRNA 5'-end processing	5.63E-30	29	364	37	6440
34471	ncRNA 5'-end processing	9.36E-28	29	364	41	6440
472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.25E-27	27	364	35	6440
966	RNA 5'-end processing	2.87E-27	29	364	42	6440
480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4.52E-27	26	364	33	6440

6139	nucleobase-containing compound metabolic process	2.53E-26	200	364	1876	6440
470	maturation of LSU-rRNA	3.75E-25	32	364	59	6440
6725	cellular aromatic compound metabolic process	7.64E-25	203	364	1968	6440
463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.92E-24	28	364	45	6440
46483	heterocycle metabolic process	4.17E-24	202	364	1976	6440
90304	nucleic acid metabolic process	3.19E-23	177	364	1626	6440
1901360	organic cyclic compound metabolic process	8.53E-23	203	364	2035	6440
90502	RNA phosphodiester bond hydrolysis, endonucleolytic	2.84E-18	40	364	142	6440
90501	RNA phosphodiester bond hydrolysis	1.64E-17	46	364	195	6440
10467	gene expression	5.18E-17	180	364	1883	6440
71840	cellular component organization or biogenesis	9.89E-17	207	364	2328	6440
90305	nucleic acid phosphodiester bond hydrolysis	4.58E-13	48	364	271	6440
34641	cellular nitrogen compound metabolic process	4.71E-13	213	364	2598	6440
27	ribosomal large subunit assembly	3.80E-12	18	364	43	6440
54	ribosomal subunit export from nucleus	4.88E-12	19	364	49	6440
33750	ribosome localization	7.47E-12	19	364	50	6440
9451	RNA modification	2.53E-11	36	364	184	6440
42255	ribosome assembly	4.69E-11	23	364	81	6440
71428	rRNA-containing ribonucleoprotein complex export from nucleus	1.03E-09	19	364	64	6440
154	rRNA modification	2.39E-09	23	364	97	6440
10501	RNA secondary structure unwinding	2.42E-09	13	364	30	6440
55	ribosomal large subunit export from nucleus	1.92E-08	12	364	29	6440
71426	ribonucleoprotein complex export from nucleus	3.89E-08	25	364	129	6440
71166	ribonucleoprotein complex localization	4.57E-08	25	364	130	6440
6611	protein export from nucleus	5.36E-08	25	364	131	6440
6405	RNA export from nucleus	6.28E-08	25	364	132	6440
51168	nuclear export	8.56E-08	25	364	134	6440
6913	nucleocytoplasmic transport	1.34E-07	29	364	176	6440
51169	nuclear transport	1.34E-07	29	364	176	6440
22618	ribonucleoprotein complex assembly	2.14E-07	30	364	190	6440
71826	ribonucleoprotein complex subunit organization	2.58E-07	31	364	202	6440
1522	pseudouridine synthesis	6.79E-07	13	364	45	6440
44238	primary metabolic process	1.21E-06	252	364	3697	6440

51236	establishment of RNA localization	1.87E-06	26	364	167	6440
50658	RNA transport	1.87E-06	26	364	167	6440
31118	rRNA pseudouridine synthesis	1.97E-06	11	364	35	6440
50657	nucleic acid transport	2.36E-06	26	364	169	6440
31503	protein-containing complex localization	3.12E-06	25	364	161	6440
6403	RNA localization	3.43E-06	27	364	183	6440
1902626	assembly of large subunit precursor of preribosome	5.42E-06	6	364	10	6440
98781	ncRNA transcription	6.47E-06	13	364	54	6440
44237	cellular metabolic process	1.70E-05	258	364	3903	6440
15931	nucleobase-containing compound transport	1.96E-05	28	364	212	6440
42790	nucleolar large rRNA transcription by RNA polymerase I	2.07E-05	7	364	17	6440
6807	nitrogen compound metabolic process	2.80E-05	234	364	3478	6440
51656	establishment of organelle localization	3.15E-05	20	364	129	6440
8152	metabolic process	3.43E-05	267	364	4100	6440
6099	tricarboxylic acid cycle	3.54E-05	9	364	31	6440
6101	citrate metabolic process	3.54E-05	9	364	31	6440
72350	tricarboxylic acid metabolic process	4.68E-05	9	364	32	6440
71704	organic substance metabolic process	6.26E-05	253	364	3860	6440
16074	snoRNA metabolic process	8.85E-05	12	364	59	6440
70925	organelle assembly	1.18E-04	23	364	175	6440
6360	transcription by RNA polymerase I	1.61E-04	9	364	37	6440
9060	aerobic respiration	1.73E-04	15	364	92	6440
6577	amino-acid betaine metabolic process	1.79E-04	3	364	3	6440
464	endonucleolytic cleavage in ITS1 upstream of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.79E-04	3	364	3	6440
9437	carnitine metabolic process	1.79E-04	3	364	3	6440
9303	rRNA transcription	1.88E-04	8	364	30	6440
1510	RNA methylation	2.55E-04	14	364	85	6440
45943	positive regulation of transcription by RNA polymerase I	2.60E-04	7	364	24	6440
31120	snRNA pseudouridine synthesis	3.07E-04	4	364	7	6440
70475	rRNA base methylation	3.07E-04	4	364	7	6440
40031	snRNA modification	3.07E-04	4	364	7	6440
6399	tRNA metabolic process	4.02E-04	24	364	202	6440
6400	tRNA modification	4.25E-04	13	364	79	6440

19541	propionate metabolic process	6.87E-04	3	364	4	6440
43414	macromolecule methylation	8.04E-04	17	364	128	6440
32259	methylation	9.34E-04	19	364	153	6440
6097	glyoxylate cycle	1.01E-03	4	364	9	6440
15985	energy coupled proton transport, down electrochemical gradient	1.08E-03	6	364	22	6440
15986	ATP synthesis coupled proton transport	1.08E-03	6	364	22	6440
45333	cellular respiration	1.12E-03	15	364	109	6440
30488	tRNA methylation	1.39E-03	6	364	23	6440
16073	snRNA metabolic process	1.40E-03	7	364	31	6440
43170	macromolecule metabolic process	1.54E-03	199	364	3027	6440
46487	glyoxylate metabolic process	1.61E-03	4	364	10	6440
6356	regulation of transcription by RNA polymerase I	1.78E-03	8	364	41	6440
9161	ribonucleoside monophosphate metabolic process	1.87E-03	17	364	138	6440
6631	fatty acid metabolic process	1.99E-03	10	364	61	6440
9199	ribonucleoside triphosphate metabolic process	2.20E-03	14	364	105	6440
51259	protein complex oligomerization	2.61E-03	5	364	18	6440
42797	tRNA transcription by RNA polymerase III	2.61E-03	5	364	18	6440
9123	nucleoside monophosphate metabolic process	2.75E-03	17	364	143	6440
19693	ribose phosphate metabolic process	2.82E-03	19	364	168	6440
1901657	glycosyl compound metabolic process	2.95E-03	9	364	54	6440
46459	short-chain fatty acid metabolic process	3.15E-03	3	364	6	6440
34964	box H/ACA snoRNA processing	3.19E-03	2	364	2	6440
465	exonucleolytic trimming to generate mature 5'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.19E-03	2	364	2	6440
493	box H/ACA snoRNP assembly	3.19E-03	2	364	2	6440
33979	box H/ACA snoRNA metabolic process	3.19E-03	2	364	2	6440
15864	pyrimidine nucleoside transport	3.19E-03	2	364	2	6440
34462	small-subunit processome assembly	3.19E-03	2	364	2	6440
6106	fumarate metabolic process	3.19E-03	2	364	2	6440
9304	tRNA transcription	3.38E-03	5	364	19	6440
42407	cristae formation	3.46E-03	4	364	12	6440
9156	ribonucleoside monophosphate biosynthetic process	3.70E-03	12	364	88	6440

Table 4-A11. Full Gene Ontology terms based on up-regulated differentially expressed genes at 1 h in the MS300c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
42908	xenobiotic transport	1.11E-06	3	32	5	6440
9069	serine family amino acid metabolic process	4.47E-05	4	32	41	6440
19344	cysteine biosynthetic process	8.65E-05	3	32	18	6440
6534	cysteine metabolic process	1.20E-04	3	32	20	6440
9070	serine family amino acid biosynthetic process	4.56E-04	3	32	31	6440
71266	de novo' L-methionine biosynthetic process	6.57E-04	2	32	8	6440
9066	aspartate family amino acid metabolic process	6.69E-04	4	32	82	6440
19343	cysteine biosynthetic process via cystathionine	8.43E-04	2	32	9	6440
19346	transsulfuration	8.43E-04	2	32	9	6440
9086	methionine biosynthetic process	9.02E-04	3	32	39	6440
97	sulfur amino acid biosynthetic process	1.05E-03	3	32	41	6440
6555	methionine metabolic process	1.29E-03	3	32	44	6440
6855	drug transmembrane transport	1.37E-03	3	32	45	6440
50667	homocysteine metabolic process	1.53E-03	2	32	12	6440
96	sulfur amino acid metabolic process	1.56E-03	3	32	47	6440

Table 4-A12. Full Gene Ontology terms based on down-regulated differentially expressed genes at 1 h in the MS300c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
34306	regulation of sexual sporulation	1.40E-03	1	3	3	6440
43940	regulation of sexual sporulation resulting in formation of a cellular spore	1.40E-03	1	3	3	6440
43942	negative regulation of sexual sporulation resulting in formation of a cellular spore	1.40E-03	1	3	3	6440
2001040	positive regulation of cellular response to drug	1.86E-03	1	3	4	6440
43939	negative regulation of sporulation	1.86E-03	1	3	4	6440
42174	negative regulation of sporulation resulting in formation of a cellular spore	1.86E-03	1	3	4	6440
45596	negative regulation of cell differentiation	2.33E-03	1	3	5	6440
43901	negative regulation of multi-organism process	2.33E-03	1	3	5	6440
2001038	regulation of cellular response to drug	2.33E-03	1	3	5	6440
2001025	positive regulation of response to drug	2.33E-03	1	3	5	6440
42173	regulation of sporulation resulting in formation of a cellular spore	2.33E-03	1	3	5	6440
2001023	regulation of response to drug	2.79E-03	1	3	6	6440
43937	regulation of sporulation	3.26E-03	1	3	7	6440
51093	negative regulation of developmental process	4.65E-03	1	3	10	6440

Table 4-A13. Full Gene Ontology terms based on up-regulated differentially expressed genes at 4 h in the MS300c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
42254	ribosome biogenesis	2.00E-110	223	625	477	6440
22613	ribonucleoprotein complex biogenesis	5.61E-101	234	625	572	6440
2181	cytoplasmic translation	1.86E-90	130	625	189	6440
34660	ncRNA metabolic process	3.87E-79	212	625	579	6440
16072	rRNA metabolic process	5.70E-74	170	625	398	6440
6364	rRNA processing	1.05E-73	160	625	354	6440
34470	ncRNA processing	1.03E-70	182	625	473	6440
42274	ribosomal small subunit biogenesis	1.60E-65	98	625	147	6440
42273	ribosomal large subunit biogenesis	3.62E-59	86	625	125	6440
10467	gene expression	4.51E-59	367	625	1883	6440
30490	maturation of SSU-rRNA	1.16E-54	81	625	120	6440
462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2.12E-53	76	625	108	6440
6396	RNA processing	1.07E-52	192	625	654	6440
44085	cellular component biogenesis	3.80E-46	263	625	1213	6440
34641	cellular nitrogen compound metabolic process	3.49E-45	418	625	2598	6440
42255	ribosome assembly	6.57E-43	59	625	81	6440
16070	RNA metabolic process	2.37E-38	265	625	1341	6440
460	maturation of 5.8S rRNA	3.42E-36	57	625	90	6440
466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2.42E-35	56	625	89	6440
6412	translation	7.45E-35	171	625	696	6440
43043	peptide biosynthetic process	1.65E-34	171	625	700	6440
43604	amide biosynthetic process	6.77E-34	177	625	748	6440
6518	peptide metabolic process	9.08E-32	172	625	740	6440
6807	nitrogen compound metabolic process	1.72E-31	472	625	3478	6440
1901360	organic cyclic compound metabolic process	2.98E-30	328	625	2035	6440
90304	nucleic acid metabolic process	3.60E-30	282	625	1626	6440
71826	ribonucleoprotein complex subunit organization	4.37E-30	79	625	202	6440
470	maturation of LSU-rRNA	4.51E-30	42	625	59	6440
478	endonucleolytic cleavage involved in rRNA processing	4.51E-30	42	625	59	6440

479	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4.51E-30	42	625	59	6440
22618	ribonucleoprotein complex assembly	1.00E-29	76	625	190	6440
6725	cellular aromatic compound metabolic process	1.57E-29	319	625	1968	6440
469	cleavage involved in rRNA processing	1.70E-29	49	625	82	6440
43603	cellular amide metabolic process	2.14E-29	179	625	821	6440
6139	nucleobase-containing compound metabolic process	3.63E-29	308	625	1876	6440
463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.12E-29	36	625	45	6440
46483	heterocycle metabolic process	2.49E-28	317	625	1976	6440
44238	primary metabolic process	1.93E-27	482	625	3697	6440
1901566	organonitrogen compound biosynthetic process	1.01E-26	226	625	1224	6440
71704	organic substance metabolic process	3.49E-26	493	625	3860	6440
43170	macromolecule metabolic process	3.02E-25	416	625	3027	6440
9058	biosynthetic process	1.72E-24	331	625	2197	6440
44237	cellular metabolic process	3.30E-24	492	625	3903	6440
447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.13E-24	33	625	46	6440
44271	cellular nitrogen compound biosynthetic process	2.63E-23	265	625	1623	6440
8152	metabolic process	3.51E-23	506	625	4100	6440
1901576	organic substance biosynthetic process	6.36E-23	325	625	2180	6440
27	ribosomal large subunit assembly	9.89E-23	31	625	43	6440
44249	cellular biosynthetic process	1.82E-22	321	625	2154	6440
70925	organelle assembly	8.30E-22	63	625	175	6440
71428	rRNA-containing ribonucleoprotein complex export from nucleus	8.31E-22	37	625	64	6440
480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.99E-19	25	625	33	6440
34645	cellular macromolecule biosynthetic process	3.86E-19	255	625	1635	6440
9059	macromolecule biosynthetic process	4.62E-19	255	625	1637	6440
967	rRNA 5'-end processing	8.64E-19	26	625	37	6440
28	ribosomal small subunit assembly	9.36E-19	23	625	29	6440
472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2.18E-18	25	625	35	6440

71426	ribonucleoprotein complex export from nucleus	2.71E-18	49	625	129	6440
71166	ribonucleoprotein complex localization	3.97E-18	49	625	130	6440
6611	protein export from nucleus	5.77E-18	49	625	131	6440
6405	RNA export from nucleus	8.36E-18	49	625	132	6440
51168	nuclear export	1.73E-17	49	625	134	6440
34471	ncRNA 5'-end processing	4.40E-17	26	625	41	6440
71840	cellular component organization or biogenesis	1.03E-16	322	625	2328	6440
966	RNA 5'-end processing	1.05E-16	26	625	42	6440
31503	protein-containing complex localization	7.77E-16	52	625	161	6440
51169	nuclear transport	2.54E-15	54	625	176	6440
6913	nucleocytoplasmic transport	2.54E-15	54	625	176	6440
90501	RNA phosphodiester bond hydrolysis	4.53E-15	57	625	195	6440
50658	RNA transport	1.95E-14	51	625	167	6440
51236	establishment of RNA localization	1.95E-14	51	625	167	6440
50657	nucleic acid transport	3.32E-14	51	625	169	6440
6403	RNA localization	6.69E-14	53	625	183	6440
90502	RNA phosphodiester bond hydrolysis, endonucleolytic	1.63E-13	45	625	142	6440
54	ribosomal subunit export from nucleus	2.01E-13	25	625	49	6440
33750	ribosome localization	3.65E-13	25	625	50	6440
43933	protein-containing complex subunit organization	2.75E-12	117	625	648	6440
51029	rRNA transport	1.22E-11	14	625	18	6440
6407	rRNA export from nucleus	1.22E-11	14	625	18	6440
15931	nucleobase-containing compound transport	3.81E-11	53	625	212	6440
97064	ncRNA export from nucleus	1.19E-10	18	625	33	6440
90305	nucleic acid phosphodiester bond hydrolysis	1.35E-10	61	625	271	6440
6399	tRNA metabolic process	6.70E-10	49	625	202	6440
44267	cellular protein metabolic process	2.13E-09	216	625	1581	6440
34622	cellular protein-containing complex assembly	2.54E-09	93	625	527	6440
65003	protein-containing complex assembly	5.75E-09	94	625	543	6440
9987	cellular process	1.21E-08	549	625	5130	6440
6415	translational termination	1.84E-08	11	625	16	6440
1901564	organonitrogen compound metabolic process	6.55E-08	283	625	2284	6440
55	ribosomal large subunit export from nucleus	1.11E-07	14	625	29	6440
19538	protein metabolic process	2.01E-07	221	625	1710	6440
6450	regulation of translational fidelity	5.12E-07	14	625	32	6440

44260	cellular macromolecule metabolic process	6.46E-07	307	625	2573	6440
10501	RNA secondary structure unwinding	1.51E-06	13	625	30	6440
32984	protein-containing complex disassembly	4.86E-06	20	625	69	6440
1902626	assembly of large subunit precursor of preribosome	7.26E-06	7	625	10	6440
461	endonucleolytic cleavage to generate mature 3'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	8.49E-06	5	625	5	6440
6418	tRNA aminoacylation for protein translation	8.59E-06	14	625	39	6440
9092	homoserine metabolic process	1.33E-05	8	625	14	6440
43038	amino acid activation	2.28E-05	14	625	42	6440
43039	tRNA aminoacylation	2.28E-05	14	625	42	6440
6520	cellular amino acid metabolic process	2.36E-05	47	625	264	6440
31125	rRNA 3'-end processing	2.45E-05	10	625	23	6440
43628	ncRNA 3'-end processing	3.09E-05	14	625	43	6440
6555	methionine metabolic process	4.13E-05	14	625	44	6440
2183	cytoplasmic translational initiation	4.54E-05	9	625	20	6440
51656	establishment of organelle localization	8.54E-05	27	625	129	6440
96	sulfur amino acid metabolic process	9.33E-05	14	625	47	6440
6886	intracellular protein transport	9.55E-05	71	625	474	6440
22607	cellular component assembly	1.24E-04	106	625	782	6440
98781	ncRNA transcription	1.28E-04	15	625	54	6440
43624	cellular protein complex disassembly	2.34E-04	11	625	34	6440
1902299	pre-replicative complex assembly involved in cell cycle DNA replication	3.29E-04	8	625	20	6440
6267	pre-replicative complex assembly involved in nuclear cell cycle DNA replication	3.29E-04	8	625	20	6440
36388	pre-replicative complex assembly	3.29E-04	8	625	20	6440
71266	de novo' L-methionine biosynthetic process	3.70E-04	5	625	8	6440
34248	regulation of cellular amide metabolic process	3.86E-04	28	625	148	6440
6400	tRNA modification	4.35E-04	18	625	79	6440
6448	regulation of translational elongation	6.39E-04	7	625	17	6440
45727	positive regulation of translation	7.18E-04	12	625	44	6440
448	cleavage in ITS2 between 5.8S rRNA and LSU-rRNA of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	7.66E-04	5	625	9	6440
19343	cysteine biosynthetic process via cystathionine	7.66E-04	5	625	9	6440

19346	transsulfuration	7.66E-04	5	625	9	6440
46031	ADP metabolic process	8.07E-04	10	625	33	6440
31123	RNA 3'-end processing	8.61E-04	16	625	70	6440
9086	methionine biosynthetic process	8.75E-04	11	625	39	6440
34250	positive regulation of cellular amide metabolic process	8.95E-04	12	625	45	6440
46898	response to cycloheximide	9.10E-04	3	625	3	6440
6438	valyl-tRNA aminoacylation	9.10E-04	3	625	3	6440
60992	response to fungicide	9.10E-04	3	625	3	6440
6417	regulation of translation	9.23E-04	26	625	141	6440
71265	L-methionine biosynthetic process	9.60E-04	7	625	18	6440
42797	tRNA transcription by RNA polymerase III	9.60E-04	7	625	18	6440
9135	purine nucleoside diphosphate metabolic process	1.05E-03	10	625	34	6440
9179	purine ribonucleoside diphosphate metabolic process	1.05E-03	10	625	34	6440
9185	ribonucleoside diphosphate metabolic process	1.05E-03	10	625	34	6440
9088	threonine biosynthetic process	1.12E-03	4	625	6	6440
46500	S-adenosylmethionine metabolic process	1.12E-03	4	625	6	6440
6452	translational frameshifting	1.12E-03	4	625	6	6440
1990481	mRNA pseudouridine synthesis	1.12E-03	4	625	6	6440
34655	nucleobase-containing compound catabolic process	1.33E-03	30	625	175	6440
46939	nucleotide phosphorylation	1.34E-03	10	625	35	6440
44786	cell cycle DNA replication	1.34E-03	10	625	35	6440
97	sulfur amino acid biosynthetic process	1.38E-03	11	625	41	6440
9304	tRNA transcription	1.39E-03	7	625	19	6440
45903	positive regulation of translational fidelity	1.41E-03	5	625	10	6440
2097	tRNA wobble base modification	1.59E-03	9	625	30	6440
44270	cellular nitrogen compound catabolic process	1.67E-03	33	625	201	6440
46394	carboxylic acid biosynthetic process	1.67E-03	35	625	217	6440
16053	organic acid biosynthetic process	1.67E-03	35	625	217	6440
9066	aspartate family amino acid metabolic process	1.90E-03	17	625	82	6440
6413	translational initiation	2.02E-03	14	625	62	6440
9132	nucleoside diphosphate metabolic process	2.13E-03	10	625	37	6440
6360	transcription by RNA polymerase I	2.13E-03	10	625	37	6440
9067	aspartate family amino acid biosynthetic process	2.22E-03	13	625	56	6440
8033	tRNA processing	2.28E-03	23	625	127	6440
6573	valine metabolic process	2.38E-03	5	625	11	6440

9099	valine biosynthetic process	2.42E-03	4	625	7	6440
51083	de novo' cotranslational protein folding	2.42E-03	4	625	7	6440
19752	carboxylic acid metabolic process	2.46E-03	60	625	433	6440
6090	pyruvate metabolic process	2.56E-03	11	625	44	6440
19439	aromatic compound catabolic process	2.74E-03	32	625	199	6440
10608	posttranscriptional regulation of gene expression	2.82E-03	26	625	152	6440
46700	heterocycle catabolic process	3.21E-03	32	625	201	6440
6354	DNA-templated transcription, elongation	3.22E-03	14	625	65	6440
1901654	response to ketone	3.38E-03	3	625	4	6440
1732	formation of cytoplasmic translation initiation complex	3.38E-03	3	625	4	6440
6432	phenylalanyl-tRNA aminoacylation	3.38E-03	3	625	4	6440
8652	cellular amino acid biosynthetic process	3.44E-03	23	625	131	6440
50667	homocysteine metabolic process	3.76E-03	5	625	12	6440
6549	isoleucine metabolic process	3.76E-03	5	625	12	6440

Table 4-A14. Full Gene Ontology terms based on down-regulated differentially expressed genes at 4 h in the MS300c strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
32787	monocarboxylic acid metabolic process	3.85E-10	37	430	180	6440
55114	oxidation-reduction process	6.55E-10	65	430	446	6440
19752	carboxylic acid metabolic process	9.12E-09	61	430	433	6440
46942	carboxylic acid transport	9.54E-09	24	430	96	6440
15849	organic acid transport	1.48E-08	24	430	98	6440
43436	oxoacid metabolic process	1.77E-08	62	430	451	6440
6082	organic acid metabolic process	2.10E-08	62	430	453	6440
6811	ion transport	2.22E-08	56	430	391	6440
44281	small molecule metabolic process	2.84E-08	91	430	782	6440
34220	ion transmembrane transport	4.70E-08	43	430	269	6440
15980	energy derivation by oxidation of organic compounds	7.98E-08	30	430	155	6440
46395	carboxylic acid catabolic process	1.75E-07	22	430	95	6440
16054	organic acid catabolic process	2.13E-07	22	430	96	6440
6091	generation of precursor metabolites and energy	2.23E-07	35	430	207	6440
6631	fatty acid metabolic process	2.65E-07	17	430	61	6440
5975	carbohydrate metabolic process	4.08E-07	40	430	260	6440
44262	cellular carbohydrate metabolic process	4.33E-07	29	430	158	6440
9060	aerobic respiration	4.34E-07	21	430	92	6440
44282	small molecule catabolic process	1.08E-06	27	430	147	6440
15718	monocarboxylic acid transport	1.33E-06	10	430	24	6440
55085	transmembrane transport	1.37E-06	58	430	463	6440
31118	rRNA pseudouridine synthesis	1.37E-06	12	430	35	6440
72329	monocarboxylic acid catabolic process	2.20E-06	14	430	49	6440
44242	cellular lipid catabolic process	4.45E-06	13	430	45	6440
9062	fatty acid catabolic process	5.52E-06	9	430	22	6440
5978	glycogen biosynthetic process	6.80E-06	7	430	13	6440
45333	cellular respiration	7.96E-06	21	430	109	6440
16051	carbohydrate biosynthetic process	1.27E-05	18	430	87	6440
98656	anion transmembrane transport	1.44E-05	19	430	96	6440
6820	anion transport	1.99E-05	29	430	190	6440
15711	organic anion transport	2.20E-05	26	430	162	6440

33692	cellular polysaccharide biosynthetic process	2.51E-05	13	430	52	6440
1522	pseudouridine synthesis	2.56E-05	12	430	45	6440
271	polysaccharide biosynthetic process	3.13E-05	13	430	53	6440
17144	drug metabolic process	3.36E-05	36	430	267	6440
9250	glucan biosynthetic process	3.64E-05	10	430	33	6440
46323	glucose import	3.64E-05	10	430	33	6440
1904659	glucose transmembrane transport	4.85E-05	10	430	34	6440
8645	hexose transmembrane transport	4.85E-05	10	430	34	6440
15749	monosaccharide transmembrane transport	4.85E-05	10	430	34	6440
34637	cellular carbohydrate biosynthetic process	5.13E-05	14	430	63	6440
6119	oxidative phosphorylation	5.24E-05	11	430	41	6440
34219	carbohydrate transmembrane transport	6.39E-05	10	430	35	6440
42737	drug catabolic process	8.44E-05	11	430	43	6440
6122	mitochondrial electron transport, ubiquinol to cytochrome c	9.81E-05	6	430	13	6440
1905039	carboxylic acid transmembrane transport	1.04E-04	13	430	59	6440
16042	lipid catabolic process	1.25E-04	13	430	60	6440
1903825	organic acid transmembrane transport	1.49E-04	13	430	61	6440
8643	carbohydrate transport	1.63E-04	11	430	46	6440
42773	ATP synthesis coupled electron transport	1.74E-04	10	430	39	6440
42775	mitochondrial ATP synthesis coupled electron transport	1.74E-04	10	430	39	6440
6812	cation transport	2.20E-04	30	430	227	6440
19740	nitrogen utilization	2.47E-04	5	430	10	6440
98655	cation transmembrane transport	2.80E-04	26	430	188	6440
42183	formate catabolic process	2.96E-04	3	430	3	6440
9437	carnitine metabolic process	2.96E-04	3	430	3	6440
6577	amino-acid betaine metabolic process	2.96E-04	3	430	3	6440
15942	formate metabolic process	2.96E-04	3	430	3	6440
44264	cellular polysaccharide metabolic process	3.18E-04	14	430	74	6440
19953	sexual reproduction	4.19E-04	24	430	172	6440
44703	multi-organism reproductive process	4.19E-04	24	430	172	6440
51704	multi-organism process	4.26E-04	26	430	193	6440
48856	anatomical structure development	5.16E-04	27	430	206	6440
22413	reproductive process in single-celled organism	5.25E-04	21	430	144	6440
15696	ammonium transport	5.40E-04	7	430	23	6440
3006	developmental process involved in reproduction	6.23E-04	22	430	156	6440

6635	fatty acid beta-oxidation	6.93E-04	5	430	12	6440
5984	disaccharide metabolic process	7.44E-04	8	430	31	6440
6099	tricarboxylic acid cycle	7.44E-04	8	430	31	6440
6101	citrate metabolic process	7.44E-04	8	430	31	6440
34293	sexual sporulation	8.37E-04	18	430	119	6440
43935	sexual sporulation resulting in formation of a cellular spore	8.37E-04	18	430	119	6440
22904	respiratory electron transport chain	8.74E-04	10	430	47	6440
30435	sporulation resulting in formation of a cellular spore	9.25E-04	23	430	171	6440
6112	energy reserve metabolic process	9.35E-04	8	430	32	6440
72350	tricarboxylic acid metabolic process	9.35E-04	8	430	32	6440
43934	sporulation	1.00E-03	23	430	172	6440
71852	fungal-type cell wall organization or biogenesis	1.01E-03	28	430	226	6440
48646	anatomical structure formation involved in morphogenesis	1.09E-03	23	430	173	6440
71361	cellular response to ethanol	1.11E-03	4	430	8	6440
97306	cellular response to alcohol	1.11E-03	4	430	8	6440
19541	propionate metabolic process	1.12E-03	3	430	4	6440
9653	anatomical structure morphogenesis	1.42E-03	25	430	198	6440
30437	ascospore formation	1.50E-03	17	430	115	6440
34440	lipid oxidation	1.57E-03	5	430	14	6440
19395	fatty acid oxidation	1.57E-03	5	430	14	6440
48468	cell development	1.65E-03	17	430	116	6440
5976	polysaccharide metabolic process	1.70E-03	14	430	87	6440
6097	glyoxylate cycle	1.89E-03	4	430	9	6440
9311	oligosaccharide metabolic process	2.13E-03	8	430	36	6440

Table 4-A15. Full Gene Ontology terms based on up-regulated differentially expressed genes at 1 h in the MS300c- strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
42908	xenobiotic transport	7.32E-07	3	28	5	6440
46618	drug export	9.29E-05	3	28	21	6440
42493	response to drug	1.95E-04	5	28	128	6440
35690	cellular response to drug	2.49E-04	3	28	29	6440
15893	drug transport	3.27E-04	4	28	78	6440

Table 4-A16. Full Gene Ontology terms based on down-regulated differentially expressed genes at 1 h in the MS300c- strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
90368	regulation of ornithine metabolic process	1.24E-03	1	8	1	6440
51510	regulation of unidimensional cell growth	1.24E-03	1	8	1	6440
51512	positive regulation of unidimensional cell growth	1.24E-03	1	8	1	6440
51513	regulation of monopolar cell growth	1.24E-03	1	8	1	6440
51515	positive regulation of monopolar cell growth	1.24E-03	1	8	1	6440
19547	arginine catabolic process to ornithine	1.24E-03	1	8	1	6440
48638	regulation of developmental growth	1.24E-03	1	8	1	6440
48639	positive regulation of developmental growth	1.24E-03	1	8	1	6440
6527	arginine catabolic process	2.48E-03	1	8	2	6440

Table 4-A17. Full Gene Ontology terms based on up-regulated differentially expressed genes at 4 h in the MS300c- strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
2181	cytoplasmic translation	2.50E-92	130	606	189	6440
42254	ribosome biogenesis	2.70E-74	184	606	477	6440
22613	ribonucleoprotein complex biogenesis	7.89E-62	187	606	572	6440
6364	rRNA processing	4.59E-48	130	606	354	6440
16072	rRNA metabolic process	2.36E-45	135	606	398	6440
42274	ribosomal small subunit biogenesis	1.48E-43	79	606	147	6440
34470	ncRNA processing	7.53E-43	145	606	473	6440
42273	ribosomal large subunit biogenesis	3.39E-40	70	606	125	6440
34660	ncRNA metabolic process	1.73E-38	156	606	579	6440
462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.64E-36	62	606	108	6440
30490	maturation of SSU-rRNA	4.83E-35	64	606	120	6440
42255	ribosome assembly	3.36E-34	52	606	81	6440
6412	translation	7.16E-30	159	606	696	6440
43604	amide biosynthetic process	1.05E-29	166	606	748	6440
43043	peptide biosynthetic process	1.46E-29	159	606	700	6440
6396	RNA processing	1.10E-27	149	606	654	6440
6518	peptide metabolic process	3.86E-27	160	606	740	6440
43603	cellular amide metabolic process	3.68E-26	169	606	821	6440
44085	cellular component biogenesis	1.19E-24	215	606	1213	6440
10467	gene expression	1.96E-24	290	606	1883	6440
1901566	organonitrogen compound biosynthetic process	5.03E-22	210	606	1224	6440
470	maturation of LSU-rRNA	2.24E-19	33	606	59	6440
27	ribosomal large subunit assembly	7.01E-18	27	606	43	6440
28	ribosomal small subunit assembly	1.53E-17	22	606	29	6440
463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.78E-17	27	606	45	6440
71428	rRNA-containing ribonucleoprotein complex export from nucleus	6.69E-17	32	606	64	6440
460	maturation of 5.8S rRNA	1.07E-16	38	606	90	6440
22618	ribonucleoprotein complex assembly	3.04E-16	57	606	190	6440

70925	organelle assembly	4.98E-16	54	606	175	6440
466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.07E-16	37	606	89	6440
71826	ribonucleoprotein complex subunit organization	1.51E-15	58	606	202	6440
478	endonucleolytic cleavage involved in rRNA processing	3.56E-15	29	606	59	6440
479	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.56E-15	29	606	59	6440
469	cleavage involved in rRNA processing	8.88E-15	34	606	82	6440
34641	cellular nitrogen compound metabolic process	1.74E-14	333	606	2598	6440
51029	rRNA transport	2.13E-13	15	606	18	6440
6407	rRNA export from nucleus	2.13E-13	15	606	18	6440
71426	ribonucleoprotein complex export from nucleus	6.55E-13	41	606	129	6440
71166	ribonucleoprotein complex localization	8.74E-13	41	606	130	6440
6611	protein export from nucleus	1.16E-12	41	606	131	6440
6405	RNA export from nucleus	1.54E-12	41	606	132	6440
51168	nuclear export	2.67E-12	41	606	134	6440
44271	cellular nitrogen compound biosynthetic process	1.83E-11	223	606	1623	6440
447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.45E-10	21	606	46	6440
9058	biosynthetic process	2.03E-10	278	606	2197	6440
16070	RNA metabolic process	3.33E-10	188	606	1341	6440
1901576	organic substance biosynthetic process	7.16E-10	274	606	2180	6440
97064	ncRNA export from nucleus	7.95E-10	17	606	33	6440
50658	RNA transport	1.43E-09	42	606	167	6440
51236	establishment of RNA localization	1.43E-09	42	606	167	6440
31503	protein-containing complex localization	1.51E-09	41	606	161	6440
50657	nucleic acid transport	2.12E-09	42	606	169	6440
51169	nuclear transport	2.38E-09	43	606	176	6440
6913	nucleocytoplasmic transport	2.38E-09	43	606	176	6440
6403	RNA localization	2.64E-09	44	606	183	6440
44249	cellular biosynthetic process	4.32E-09	268	606	2154	6440
44237	cellular metabolic process	1.60E-08	430	606	3903	6440
6807	nitrogen compound metabolic process	3.90E-08	390	606	3478	6440
8152	metabolic process	5.29E-08	445	606	4100	6440

54	ribosomal subunit export from nucleus	1.85E-07	18	606	49	6440
34645	cellular macromolecule biosynthetic process	2.55E-07	207	606	1635	6440
33750	ribosome localization	2.65E-07	18	606	50	6440
15931	nucleobase-containing compound transport	2.81E-07	44	606	212	6440
9059	macromolecule biosynthetic process	2.82E-07	207	606	1637	6440
1901564	organonitrogen compound metabolic process	3.21E-07	272	606	2284	6440
71704	organic substance metabolic process	3.32E-07	420	606	3860	6440
44238	primary metabolic process	3.89E-07	405	606	3697	6440
967	rRNA 5'-end processing	4.44E-07	15	606	37	6440
480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.55E-07	14	606	33	6440
44267	cellular protein metabolic process	8.06E-07	199	606	1581	6440
472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.31E-06	14	606	35	6440
90502	RNA phosphodiester bond hydrolysis, endonucleolytic	1.93E-06	32	606	142	6440
34471	ncRNA 5'-end processing	2.10E-06	15	606	41	6440
6450	regulation of translational fidelity	2.57E-06	13	606	32	6440
966	RNA 5'-end processing	2.99E-06	15	606	42	6440
90501	RNA phosphodiester bond hydrolysis	3.56E-06	39	606	195	6440
1902626	assembly of large subunit precursor of preribosome	5.89E-06	7	606	10	6440
9082	branched-chain amino acid biosynthetic process	6.64E-06	9	606	17	6440
461	endonucleolytic cleavage to generate mature 3'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	7.27E-06	5	606	5	6440
6139	nucleobase-containing compound metabolic process	7.51E-06	224	606	1876	6440
71840	cellular component organization or biogenesis	1.05E-05	268	606	2328	6440
90304	nucleic acid metabolic process	2.24E-05	196	606	1626	6440
19538	protein metabolic process	4.10E-05	203	606	1710	6440
6725	cellular aromatic compound metabolic process	5.68E-05	228	606	1968	6440
46483	heterocycle metabolic process	7.59E-05	228	606	1976	6440
43170	macromolecule metabolic process	9.57E-05	329	606	3027	6440
43628	ncRNA 3'-end processing	1.02E-04	13	606	43	6440
15755	fructose transmembrane transport	1.09E-04	8	606	18	6440
31125	rRNA 3'-end processing	1.33E-04	9	606	23	6440
1901360	organic cyclic compound metabolic process	1.46E-04	232	606	2035	6440
8652	cellular amino acid biosynthetic process	1.73E-04	26	606	131	6440

6520	cellular amino acid metabolic process	2.12E-04	43	606	264	6440
6415	translational termination	3.38E-04	7	606	16	6440
15761	mannose transmembrane transport	3.38E-04	7	606	16	6440
9098	leucine biosynthetic process	6.63E-04	5	606	9	6440
1904659	glucose transmembrane transport	8.21E-04	10	606	34	6440
8645	hexose transmembrane transport	8.21E-04	10	606	34	6440
15749	monosaccharide transmembrane transport	8.21E-04	10	606	34	6440
46898	response to cycloheximide	8.29E-04	3	606	3	6440
60992	response to fungicide	8.29E-04	3	606	3	6440
34622	cellular protein-containing complex assembly	9.24E-04	71	606	527	6440
1901607	alpha-amino acid biosynthetic process	9.69E-04	23	606	123	6440
46394	carboxylic acid biosynthetic process	9.73E-04	35	606	217	6440
16053	organic acid biosynthetic process	9.73E-04	35	606	217	6440
55	ribosomal large subunit export from nucleus	9.73E-04	9	606	29	6440
34219	carbohydrate transmembrane transport	1.05E-03	10	606	35	6440
19752	carboxylic acid metabolic process	1.17E-03	60	606	433	6440
9097	isoleucine biosynthetic process	1.22E-03	5	606	10	6440
9081	branched-chain amino acid metabolic process	1.28E-03	9	606	30	6440
6082	organic acid metabolic process	1.33E-03	62	606	453	6440
90305	nucleic acid phosphodiester bond hydrolysis	1.37E-03	41	606	271	6440
43436	oxoacid metabolic process	1.94E-03	61	606	451	6440
65003	protein-containing complex assembly	2.09E-03	71	606	543	6440
9099	valine biosynthetic process	2.16E-03	4	606	7	6440
46323	glucose import	2.66E-03	9	606	33	6440

Table 4-A18. Full Gene Ontology terms based on down-regulated differentially expressed genes at 4 h in the MS300c- strain.

GO ID	Description	p-value	Number of DE genes in the GO term	Total number of DE genes	Number of genes in the GO term	Total number of genes
22402	cell cycle process	3.55E-20	104	453	590	6440
7049	cell cycle	1.24E-19	118	453	733	6440
22414	reproductive process	6.46E-16	77	453	419	6440
278	mitotic cell cycle	7.86E-16	68	453	343	6440
3	reproduction	1.71E-15	78	453	435	6440
1903047	mitotic cell cycle process	4.28E-14	63	453	327	6440
747	conjugation with cellular fusion	2.50E-13	23	453	54	6440
746	conjugation	6.39E-13	23	453	56	6440
44764	multi-organism cellular process	8.08E-12	23	453	62	6440
280	nuclear division	3.79E-10	40	453	195	6440
51301	cell division	4.18E-10	52	453	298	6440
19953	sexual reproduction	4.36E-10	37	453	172	6440
44703	multi-organism reproductive process	4.36E-10	37	453	172	6440
7010	cytoskeleton organization	9.17E-10	44	453	234	6440
98813	nuclear chromosome segregation	1.33E-09	34	453	155	6440
7059	chromosome segregation	1.66E-09	38	453	188	6440
140014	mitotic nuclear division	1.78E-09	28	453	112	6440
48285	organelle fission	2.11E-09	40	453	206	6440
51704	multi-organism process	3.62E-09	38	453	193	6440
819	sister chromatid segregation	4.81E-09	29	453	124	6440
51321	meiotic cell cycle	9.14E-09	51	453	315	6440
7051	spindle organization	1.25E-08	16	453	43	6440
71554	cell wall organization or biogenesis	1.25E-08	48	453	290	6440
71852	fungal-type cell wall organization or biogenesis	3.34E-08	40	453	226	6440
7052	mitotic spindle organization	3.50E-08	14	453	35	6440
45229	external encapsulating structure organization	4.94E-08	41	453	238	6440
71555	cell wall organization	4.94E-08	41	453	238	6440
31505	fungal-type cell wall organization	1.18E-07	35	453	192	6440
7017	microtubule-based process	2.18E-07	25	453	114	6440
1903046	meiotic cell cycle process	2.82E-07	41	453	253	6440
226	microtubule cytoskeleton organization	6.38E-07	22	453	97	6440

70	mitotic sister chromatid segregation	9.26E-07	22	453	99	6440
51225	spindle assembly	1.16E-06	8	453	14	6440
33692	cellular polysaccharide biosynthetic process	1.61E-06	15	453	52	6440
16051	carbohydrate biosynthetic process	1.65E-06	20	453	87	6440
271	polysaccharide biosynthetic process	2.10E-06	15	453	53	6440
1902850	microtubule cytoskeleton organization involved in mitosis	3.11E-06	14	453	48	6440
34637	cellular carbohydrate biosynthetic process	4.62E-06	16	453	63	6440
755	cytogamy	4.73E-06	7	453	12	6440
51274	beta-glucan biosynthetic process	5.34E-06	9	453	21	6440
51726	regulation of cell cycle	6.14E-06	42	453	294	6440
32185	septin cytoskeleton organization	6.36E-06	12	453	38	6440
60236	regulation of mitotic spindle organization	8.21E-06	6	453	9	6440
31109	microtubule polymerization or depolymerization	8.48E-06	9	453	22	6440
8608	attachment of spindle microtubules to kinetochore	8.65E-06	11	453	33	6440
9250	glucan biosynthetic process	8.65E-06	11	453	33	6440
31106	septin ring organization	1.20E-05	11	453	34	6440
51273	beta-glucan metabolic process	1.31E-05	9	453	23	6440
22603	regulation of anatomical structure morphogenesis	1.53E-05	12	453	41	6440
31118	rRNA pseudouridine synthesis	1.64E-05	11	453	35	6440
90224	regulation of spindle organization	1.93E-05	6	453	10	6440
61982	meiosis I cell cycle process	2.15E-05	20	453	102	6440
22604	regulation of cell morphogenesis	2.21E-05	11	453	36	6440
5976	polysaccharide metabolic process	2.59E-05	18	453	87	6440
51278	fungal-type cell wall polysaccharide biosynthetic process	2.88E-05	9	453	25	6440
71966	fungal-type cell wall polysaccharide metabolic process	2.88E-05	9	453	25	6440
8360	regulation of cell shape	3.10E-05	10	453	31	6440
10383	cell wall polysaccharide metabolic process	3.10E-05	10	453	31	6440
742	karyogamy involved in conjugation with cellular fusion	3.19E-05	7	453	15	6440
30472	mitotic spindle organization in nucleus	3.99E-05	6	453	11	6440
44264	cellular polysaccharide metabolic process	4.12E-05	16	453	74	6440
10564	regulation of cell cycle process	4.22E-05	31	453	207	6440
70507	regulation of microtubule cytoskeleton organization	4.23E-05	10	453	32	6440
32886	regulation of microtubule-based process	5.69E-05	10	453	33	6440
6928	movement of cell or subcellular component	6.58E-05	11	453	40	6440
32505	reproduction of a single-celled organism	7.02E-05	29	453	193	6440

741	karyogamy	7.47E-05	8	453	22	6440
51128	regulation of cellular component organization	7.63E-05	54	453	456	6440
70592	cell wall polysaccharide biosynthetic process	8.04E-05	9	453	28	6440
910	cytokinesis	8.84E-05	18	453	95	6440
16043	cellular component organization	1.02E-04	174	453	1959	6440
50794	regulation of cellular process	1.09E-04	153	453	1683	6440
34407	cell wall (1->3)-beta-D-glucan metabolic process	1.14E-04	4	453	5	6440
34410	cell wall beta-glucan biosynthetic process	1.14E-04	4	453	5	6440
34411	cell wall (1->3)-beta-D-glucan biosynthetic process	1.14E-04	4	453	5	6440
71969	fungal-type cell wall (1->3)-beta-D-glucan metabolic process	1.14E-04	4	453	5	6440
71970	fungal-type cell wall (1->3)-beta-D-glucan biosynthetic process	1.14E-04	4	453	5	6440
7534	gene conversion at mating-type locus	1.14E-04	4	453	5	6440
51716	cellular response to stimulus	1.48E-04	106	453	1089	6440
7163	establishment or maintenance of cell polarity	1.63E-04	20	453	117	6440
7346	regulation of mitotic cell cycle	1.65E-04	26	453	173	6440
90307	mitotic spindle assembly	1.67E-04	5	453	9	6440
70879	fungal-type cell wall beta-glucan metabolic process	1.67E-04	5	453	9	6440
70880	fungal-type cell wall beta-glucan biosynthetic process	1.67E-04	5	453	9	6440
34406	cell wall beta-glucan metabolic process	1.67E-04	5	453	9	6440
6075	(1->3)-beta-D-glucan biosynthetic process	1.67E-04	5	453	9	6440
35822	gene conversion	1.67E-04	5	453	9	6440
46785	microtubule polymerization	1.95E-04	7	453	19	6440
1522	pseudouridine synthesis	2.10E-04	11	453	45	6440
50793	regulation of developmental process	2.11E-04	13	453	60	6440
51783	regulation of nuclear division	2.28E-04	21	453	129	6440
140013	meiotic nuclear division	2.61E-04	19	453	112	6440
44770	cell cycle phase transition	2.70E-04	16	453	86	6440
44772	mitotic cell cycle phase transition	2.70E-04	16	453	86	6440
51276	chromosome organization	2.89E-04	62	453	572	6440
753	cell morphogenesis involved in conjugation with cellular fusion	3.16E-04	5	453	10	6440
120031	plasma membrane bounded cell projection assembly	3.16E-04	5	453	10	6440
51316	attachment of spindle microtubules to kinetochore involved in meiotic chromosome segregation	3.23E-04	4	453	6	6440
51455	attachment of spindle microtubules to kinetochore involved in homologous chromosome segregation	3.23E-04	4	453	6	6440

31292	gene conversion at mating-type locus, DNA double-strand break processing	3.46E-04	3	453	3	6440
31860	telomeric 3' overhang formation	3.46E-04	3	453	3	6440
50896	response to stimulus	3.60E-04	120	453	1292	6440
6073	cellular glucan metabolic process	4.10E-04	12	453	56	6440
44042	glucan metabolic process	4.10E-04	12	453	56	6440
22413	reproductive process in single-celled organism	4.12E-04	22	453	144	6440
61640	cytoskeleton-dependent cytokinesis	5.03E-04	15	453	82	6440
30010	establishment of cell polarity	5.03E-04	15	453	82	6440
33043	regulation of organelle organization	5.08E-04	40	453	333	6440
3006	developmental process involved in reproduction	5.17E-04	23	453	156	6440
767	cell morphogenesis involved in conjugation	5.45E-04	5	453	11	6440
6074	(1->3)-beta-D-glucan metabolic process	5.45E-04	5	453	11	6440
10458	exit from mitosis	5.45E-04	5	453	11	6440
44036	cell wall macromolecule metabolic process	5.60E-04	11	453	50	6440
51493	regulation of cytoskeleton organization	5.94E-04	16	453	92	6440
7127	meiosis I	5.94E-04	16	453	92	6440
5975	carbohydrate metabolic process	6.00E-04	33	453	260	6440
7088	regulation of mitotic nuclear division	6.73E-04	16	453	93	6440
281	mitotic cytokinesis	7.15E-04	14	453	76	6440
6334	nucleosome assembly	7.40E-04	7	453	23	6440
45144	meiotic sister chromatid segregation	7.43E-04	6	453	17	6440
7018	microtubule-based movement	8.29E-04	8	453	30	6440
30031	cell projection assembly	8.81E-04	5	453	12	6440
51647	nucleus localization	9.83E-04	7	453	24	6440
7097	nuclear migration	9.83E-04	7	453	24	6440
61983	meiosis II cell cycle process	1.05E-03	6	453	18	6440
7020	microtubule nucleation	1.05E-03	6	453	18	6440
7135	meiosis II	1.05E-03	6	453	18	6440
70589	cellular component macromolecule biosynthetic process	1.31E-03	10	453	47	6440
44038	cell wall macromolecule biosynthetic process	1.31E-03	10	453	47	6440
212	meiotic spindle organization	1.31E-03	3	453	4	6440
83	regulation of transcription involved in G1/S transition of mitotic cell cycle	1.31E-03	8	453	32	6440
22	mitotic spindle elongation	1.35E-03	5	453	13	6440

120036	plasma membrane bounded cell projection organization	1.35E-03	5	453	13	6440
51231	spindle elongation	1.35E-03	5	453	13	6440
45132	meiotic chromosome segregation	1.66E-03	12	453	65	6440
19236	response to pheromone	1.73E-03	15	453	92	6440
65007	biological regulation	1.79E-03	182	453	2174	6440
50789	regulation of biological process	1.84E-03	154	453	1796	6440
71840	cellular component organization or biogenesis	1.93E-03	193	453	2328	6440
30473	nuclear migration along microtubule	1.94E-03	6	453	20	6440
40007	growth	2.38E-03	17	453	114	6440
32507	maintenance of protein location in cell	2.44E-03	8	453	35	6440
6312	mitotic recombination	2.50E-03	10	453	51	6440
6468	protein phosphorylation	2.64E-03	21	453	155	6440
30030	cell projection organization	2.80E-03	5	453	15	6440
72595	maintenance of protein localization in organelle	2.80E-03	5	453	15	6440
9653	anatomical structure morphogenesis	2.90E-03	25	453	198	6440
6281	DNA repair	2.99E-03	34	453	297	6440
70192	chromosome organization involved in meiotic cell cycle	3.01E-03	9	453	44	6440
743	nuclear migration involved in conjugation with cellular fusion	3.11E-03	3	453	5	6440
82	G1/S transition of mitotic cell cycle	3.11E-03	11	453	61	6440
44843	cell cycle G1/S phase transition	3.11E-03	11	453	61	6440
51258	protein polymerization	3.26E-03	7	453	29	6440
99111	microtubule-based transport	3.31E-03	6	453	22	6440
72384	organelle transport along microtubule	3.31E-03	6	453	22	6440
10970	transport along microtubule	3.31E-03	6	453	22	6440

Table 4-A19. The enriched KEGG pathways based on differentially expressed genes at 1 h in the S288C strain.

Category	Term	Count	%	P-Value
Down-regulated				
KEGG	Ribosome biogenesis in eukaryotes	19	6.6	1.60E-07
KEGG	Ribosome	23	8	5.10E-05
KEGG	Pyrimidine metabolism	12	4.2	6.90E-04
KEGG	RNA polymerase	7	2.4	3.10E-03
KEGG	Steroid biosynthesis	5	1.7	8.60E-03
KEGG	Purine metabolism	11	3.8	2.00E-02
KEGG	Metabolic pathways	43	15	6.70E-02
KEGG	Citrate cycle (TCA cycle)	5	1.7	7.30E-02
Up-regulated				
KEGG	Starch and sucrose metabolism	20	6.5	8.90E-16
KEGG	Metabolic pathways	60	19.5	5.00E-08
KEGG	Galactose metabolism	10	3.2	6.70E-07
KEGG	Amino sugar and nucleotide sugar metabolism	9	2.9	8.50E-05
KEGG	Fructose and mannose metabolism	7	2.3	3.10E-04
KEGG	Biosynthesis of secondary metabolites	28	9.1	4.30E-04
KEGG	Pentose and glucuronate interconversions	6	1.9	4.70E-04
KEGG	Glycerolipid metabolism	7	2.3	8.80E-04
KEGG	Cysteine and methionine metabolism	8	2.6	1.20E-03
KEGG	Glycolysis / Gluconeogenesis	10	3.2	1.40E-03
KEGG	Carbon metabolism	14	4.5	2.40E-03
KEGG	Fatty acid degradation	5	1.6	1.10E-02
KEGG	Fatty acid biosynthesis	4	1.3	1.30E-02
KEGG	Biosynthesis of antibiotics	19	6.2	1.40E-02
KEGG	Fatty acid metabolism	5	1.6	1.90E-02
KEGG	Protein processing in endoplasmic reticulum	10	3.2	2.00E-02
KEGG	Histidine metabolism	4	1.3	2.10E-02
KEGG	beta-Alanine metabolism	4	1.3	2.10E-02
KEGG	Pentose phosphate pathway	5	1.6	4.20E-02
KEGG	Tryptophan metabolism	4	1.3	4.40E-02
KEGG	Arginine and proline metabolism	4	1.3	7.60E-02

Table 4-A20. The enriched KEGG pathways based on differentially expressed genes at 4 h in the S288C strain.

Category Down-regulated	Term	Count	%	P-Value
KEGG	Biosynthesis of antibiotics	44	8.4	3.40E-07
KEGG	Pyrimidine metabolism	21	4	3.20E-06
KEGG	DNA replication	13	2.5	7.90E-06
KEGG	Ribosome biogenesis in eukaryotes	23	4.4	8.40E-06
KEGG	Purine metabolism	24	4.6	9.10E-06
KEGG	Metabolic pathways	92	17.5	1.00E-05
KEGG	Carbon metabolism	26	4.9	1.90E-05
KEGG	Biosynthesis of secondary metabolites	48	9.1	4.90E-05
KEGG	Cell cycle - yeast	25	4.8	1.80E-04
KEGG	Base excision repair	8	1.5	6.70E-04
KEGG	Biosynthesis of amino acids	23	4.4	1.40E-03
KEGG	Glyoxylate and dicarboxylate metabolism	9	1.7	1.60E-03
KEGG	Mismatch repair	7	1.3	7.30E-03
KEGG	Methane metabolism	8	1.5	1.10E-02
KEGG	Glycolysis / Gluconeogenesis	12	2.3	1.40E-02
KEGG	Steroid biosynthesis	6	1.1	1.60E-02
KEGG	RNA polymerase	8	1.5	1.60E-02
KEGG	Pyruvate metabolism	9	1.7	2.30E-02
KEGG	Citrate cycle (TCA cycle)	8	1.5	2.30E-02
KEGG	Thiamine metabolism	4	0.8	5.70E-02
KEGG	Meiosis - yeast	18	3.4	6.50E-02
KEGG	2-Oxocarboxylic acid metabolism	7	1.3	9.60E-02
Up-regulated				
KEGG	Starch and sucrose metabolism	20	4.2	6.20E-13
KEGG	Metabolic pathways	69	14.5	5.40E-05
KEGG	Galactose metabolism	9	1.9	9.90E-05
KEGG	Fructose and mannose metabolism	8	1.7	2.80E-04
KEGG	Biosynthesis of secondary metabolites	36	7.5	3.10E-04
KEGG	Cysteine and methionine metabolism	10	2.1	4.20E-04
KEGG	Amino sugar and nucleotide sugar metabolism	9	1.9	8.90E-04
KEGG	Protein processing in endoplasmic reticulum	14	2.9	3.90E-03
KEGG	Carbon metabolism	15	3.1	1.80E-02
KEGG	Glycerolipid metabolism	6	1.3	2.20E-02
KEGG	Pentose phosphate pathway	6	1.3	3.50E-02
KEGG	Butanoate metabolism	4	0.8	5.10E-02
KEGG	Glycerophospholipid metabolism	6	1.3	9.70E-02

Table 4-A21. The enriched KEGG pathways based on differentially expressed genes at 4 h in the S7 strain.

Category Down-regulated	Term	Count	%	P-Value
KEGG	Ribosome biogenesis in eukaryotes	37	10.2	4.50E-25
KEGG	Carbon metabolism	21	5.8	8.90E-07
KEGG	RNA polymerase	11	3	1.40E-06
KEGG	Purine metabolism	17	4.7	2.50E-05
KEGG	Pyrimidine metabolism	14	3.9	6.50E-05
KEGG	Citrate cycle (TCA cycle)	9	2.5	1.70E-04
KEGG	Glyoxylate and dicarboxylate metabolism	8	2.2	2.70E-04
KEGG	Metabolic pathways	54	14.9	5.50E-04
KEGG	Oxidative phosphorylation	12	3.3	1.10E-03
KEGG	Biosynthesis of antibiotics	23	6.3	1.80E-03
KEGG	Biosynthesis of amino acids	15	4.1	4.40E-03
KEGG	2-Oxocarboxylic acid metabolism	7	1.9	8.80E-03
KEGG	Peroxisome	7	1.9	1.30E-02
KEGG	Pyruvate metabolism	7	1.9	1.50E-02
KEGG	Biosynthesis of secondary metabolites	24	6.6	3.20E-02
KEGG	Pentose phosphate pathway	5	1.4	5.70E-02
Up-regulated				
KEGG	Biosynthesis of antibiotics	29	14.9	3.60E-10
KEGG	Starch and sucrose metabolism	13	6.7	5.10E-09
KEGG	Biosynthesis of secondary metabolites	32	16.4	5.10E-09
KEGG	Glycolysis / Gluconeogenesis	14	7.2	5.40E-08
KEGG	Metabolic pathways	46	23.6	1.30E-06
KEGG	Galactose metabolism	8	4.1	1.30E-05
KEGG	Carbon metabolism	14	7.2	1.50E-04
KEGG	Steroid biosynthesis	5	2.6	2.60E-03
KEGG	Amino sugar and nucleotide sugar metabolism	6	3.1	5.00E-03
KEGG	Biosynthesis of amino acids	11	5.6	1.10E-02
KEGG	Pentose phosphate pathway	5	2.6	1.70E-02
KEGG	Meiosis - yeast	10	5.1	3.40E-02
KEGG	Fructose and mannose metabolism	4	2.1	3.70E-02
KEGG	Cysteine and methionine metabolism	5	2.6	3.80E-02

Table 4-A22. The enriched KEGG pathways based on differentially expressed genes at 1 h in the MS300c strain.

Category Down-regulated	Term	Count	%	P-Value
Up-regulated				
KEGG	Cysteine and methionine metabolism	3	9.4	1.10E-02
KEGG	ABC transporters	2	6.2	2.70E-02
KEGG	Biosynthesis of secondary metabolites	5	15.6	3.50E-02
KEGG	Propanoate metabolism	2	6.2	4.90E-02
KEGG	Biosynthesis of antibiotics	4	12.5	6.90E-02
KEGG	Carbon metabolism	3	9.4	9.20E-02

Table 4-A23. The enriched KEGG pathways based on differentially expressed genes at 4 h in the MS300c strain.

Category	Term	Count	%	P-Value
Down-regulated				
KEGG	Metabolic pathways	64	15	1.50E-07
KEGG	Pyruvate metabolism	13	3	3.50E-07
KEGG	Glyoxylate and dicarboxylate metabolism	10	2.3	3.70E-06
KEGG	Carbon metabolism	19	4.4	1.80E-05
KEGG	Starch and sucrose metabolism	11	2.6	2.80E-05
KEGG	Citrate cycle (TCA cycle)	9	2.1	1.80E-04
KEGG	Biosynthesis of secondary metabolites	30	7	5.20E-04
KEGG	Peroxisome	9	2.1	6.50E-04
KEGG	Fatty acid degradation	6	1.4	2.50E-03
KEGG	Biosynthesis of antibiotics	22	5.1	4.60E-03
KEGG	alpha-Linolenic acid metabolism	3	0.7	8.20E-03
KEGG	2-Oxocarboxylic acid metabolism	7	1.6	9.20E-03
KEGG	Fatty acid metabolism	5	1.2	2.70E-02
KEGG	Biosynthesis of amino acids	13	3	2.80E-02
KEGG	Histidine metabolism	4	0.9	2.90E-02
KEGG	Valine, leucine and isoleucine degradation	4	0.9	2.90E-02
KEGG	Glycerolipid metabolism	5	1.2	4.10E-02
KEGG	Pentose and glucuronate interconversions	4	0.9	4.20E-02
KEGG	Nitrogen metabolism	3	0.7	5.00E-02
KEGG	Alanine, aspartate and glutamate metabolism	5	1.2	7.20E-02
KEGG	Oxidative phosphorylation	8	1.9	8.50E-02
Up-regulated				
KEGG	Ribosome	119	19	1.50E-63
KEGG	Ribosome biogenesis in eukaryotes	35	5.6	8.40E-09
KEGG	Biosynthesis of amino acids	33	5.3	2.70E-04
KEGG	RNA polymerase	12	1.9	1.80E-03
KEGG	Cysteine and methionine metabolism	13	2.1	2.80E-03
KEGG	Purine metabolism	20	3.2	7.80E-02
KEGG	Selenocompound metabolism	5	0.8	7.80E-02
KEGG	Phenylalanine, tyrosine and tryptophan biosynthesis	6	1	8.10E-02

Table 4-A24. The enriched KEGG pathways based on differentially expressed genes at 1 h in the MS300c- strain.

Category Down-regulated	Term	Count	%	P-Value
Up-regulated KEGG	ABC transporters	2	7.1	1.90E-02

Table 4-A25. The enriched KEGG pathways based on differentially expressed genes at 4 h in the MS300c- strain.

Category Down-regulated	Term	Count	%	P-Value
KEGG	Cell cycle - yeast	28	6.2	6.40E-10
KEGG	Meiosis - yeast	20	4.4	1.20E-04
KEGG	MAPK signaling pathway - yeast	10	2.2	2.70E-03
KEGG	Terpenoid backbone biosynthesis	6	1.3	4.30E-03
KEGG	Biosynthesis of antibiotics	24	5.3	4.50E-03
KEGG	Starch and sucrose metabolism	8	1.8	8.50E-03
KEGG	Biosynthesis of secondary metabolites	28	6.2	1.40E-02
KEGG	Metabolic pathways	53	11.7	2.50E-02
KEGG	Mismatch repair	5	1.1	2.90E-02
KEGG	DNA replication	6	1.3	3.50E-02
Up-regulated				
KEGG	Ribosome	131	21.6	2.50E-83
KEGG	Ribosome biogenesis in eukaryotes	32	5.3	1.30E-07
KEGG	Valine, leucine and isoleucine biosynthesis	8	1.3	3.20E-04
KEGG	2-Oxocarboxylic acid metabolism	14	2.3	3.30E-04
KEGG	Biosynthesis of amino acids	31	5.1	5.30E-04
KEGG	Pyruvate metabolism	11	1.8	2.90E-02

국문초록

효모에서의 항바이러스제의 전사체 수준 영향에 대한연구

바이러스성 질병의 출현은 사람의 건강과 사회에 중대한 영향을 끼쳐왔다. 이러한 바이러스의 위협에 대한 대처 방법으로써 효과적이며 안전한 항바이러스 제제의 개발과 사용이 필수적이다. 현재, 약 90 종의 항바이러스제가 바이러스 감염 치료를 위해 공식적으로 허가되어 사용되고 있다. 그러나 항바이러스제가 야기할 수 있는 부작용과 그 기전은 충분히 알려져 있지 않은 실정이다. 본 논문에서는 진핵 생물의 하나인 *Saccaharomyces cerevisiae* 를 사용하여 항바이러스제로 사용되고 있는 Ribavirin 과 Nitazoxanide 가 진핵 생물에게 줄 수 있는 잠재적인 영향들을 전사체 수준에서 고찰하였다. 첫째, 2 장에서 Ribavirin 과 Nitazoxanide 가 *S. cerevisiae* killer 균주에 미치는 영향을 확인하였다. 둘째, 3 장에서 Ribavirin 이 dsRNA virus-like particles 를 가지고 있는 *S. cerevisiae* 균주의 전사체에 미치는 영향을 확인하였다. 셋째, 4 장에서 Nitazoxanide 가 dsRNA virus-like particles 을 가지고 있는 *S. cerevisiae* 균주의 전사체와 *S. cerevisiae* cured 균주의 전사체에

미치는 영향을 확인하였다. 현재까지 Ribavirin 과 Nitazoxanide 가 진핵 생물, 특히, 전체 게놈 수준에서 미치는 영향은 자세하게 규명되어 있지 않다. 따라서, RNA 시퀀싱을 기반으로 한 이 연구는 Ribavirin 과 Nitazoxanide 가 진핵 생물 전사체에 미치는 영향에 대한 이해를 제공하며 이는 이 두 가지 항바이러스제의 부작용을 규명할 수 있을 것으로 판단된다.

제 1 장에서는 이 논문의 배경 지식을 서술하였다. 또한, 항바이러스제의 안전성과 잠재적인 부작용에 대한 관련 기전을 명확하게 밝혀내기 위하여 더 많은 연구가 필요하다는 것을 설명하였다. 문헌 고찰을 통하여 이 연구에서 사용된 Ribavirin 과 Nitazoxanide 가 다른 연구자들에 의해 많이 연구 된것을 알 수 있었다. 하지만, Ribavirin 과 Nitazoxanide 가 바이러스에 감염된 숙주의 전사체에 미치는 영향에 대한 연구는 전무한 것을 확인하였다. *S. cerevisiae* 는 선행 연구들을 통해 완벽한 게놈의 파악이 가능하고 인간과 생물학적 성질을 공유하는 등의 이점 때문에 이 연구에 사용하였다. RNA 시퀀싱은 항바이러스 제제의 영향을 파악하기 위하여 사용하였다.

제 2 장에서는 *S. cerevisiae killer* 균주에 대해 Ribavirin 과 Nitazoxanide 의 효과를 시험하였다. 2 개의 항바이러스 제제는 killer 균주를 치료하기 위해 사용되었고 그 결과는 halo 분석과 전기영동 실험을 통해 확인하였다. 또한, 오염 가능성을 배제하기

위하여 interdelta PCR 도 수행하였다. 그 결과, Ribavirin 과 Nitazoxanide 는 *S. cerevisiae* killer 균주를 치료하는데 효과적이었다. 실제로, M dsRNA virus-like particles 이 killer 균주에서 제거되었다. 더불어, killer 균주가 다른 균주를 저해하는 성질을 잃어버렸고 이는 killer 균주가 가지고 있던 독소가 M dsRNA virus-like particles 에서 유래한 것을 암시한다. Interdelta PCR 의 결과를 통하여 오염 가능성도 배제하였다. 따라서 이 장에서는 *S. cerevisiae* killer 균주를 치료하는 새로운 방법을 개발하였으며 *S. cerevisiae* 를 모델로 활용하여 항바이러스 제제의 효과를 입증하기 위한 기반을 확인하였다.

제 2 장의 결과에 기반하여, 제 3 장에서는 dsRNA virus-like particles 를 가지고 있는 *S. cerevisiae* 균주의 전사체에 대한 Ribavirin 의 영향을 분석하였다. 이를 위하여 세 가지 다른 *S. cerevisiae* 균주인 S288C, S7, MS300c 가 사용되었다. Ribavirin 노출 실험은 100 uM 의 Ribavirin 을 1 시간 혹은 4 시간 동안 세 가지 균주에게 노출시키는 것으로 진행되었다. Ribavirin 에 노출된 균주와 노출하지 않은 음성 대조군에서 RNA 를 추출하여 RNA 시퀀싱을 수행하였다. 그 결과로 소핵 RNA 와 소핵소체 RNA 가 Ribavirin 에 노출된 직후 축적되었다가 줄어든 것을 확인하였다. 이 소핵 RNA 와 소핵소체 RNA 는 snRNP 또는 snoRNP 를 형성하기 위해 단백질과 결합한다. snRNPs 와 snRNPs 를 포함한

작은 RNPs 는 척수성 근위축증, 선천성 이상각화증, 프라더-윌리 증후군과 같은 인간 질병과 관련이 있는 것으로 알려져 있다. 따라서, Ribavirin 으로 치료받는 환자에게서 작은 RNPs 와 부작용 사이의 관계를 면밀히 조사할 필요가 있다.

제 3 장의 결과와 결론을 근거로 제 4 장에서는 Nitazoxanide 에 대해 연구하기로 결정하였다. Nitazoxanide 는 항바이러스제로 사용하기 위해 임상 시험 중이며 잠재적인 부작용은 아직 알려지지 않았다. 따라서 RNA 시퀀싱을 사용하여 dsRNA virus-like particles 를 가진 *S. cerevisiae* 균주와 *S. cerevisiae* cured 균주의 전사체에 대한 Nitazoxanide 의 영향을 탐색하였다. 이를 위하여 S288C, S7, MS300c 와 제 2 장에서 Ribavirin 으로 치료된 균주를 사용하였다. Nitazoxanide 노출 실험은 10 ug/ml 의 Nitazoxanide 를 4 가지 균주에 1 시간 혹은 4 시간 동안 노출시키는 것으로 진행되었다. RNA 시퀀싱은 제 3 장과 비슷한 조건으로 실행되었다. 각 균주의 RNA 시퀀싱 데이터를 음성 대조군과 비교하였을 때, Gene Ontology terms 이 강력하게 발현되었고 KEGG pathway 가 음성 대조군과 비교하여 억제되거나 촉진되었음을 확인하였다. 이 결과는 Nitazoxanide 에 노출된 *S. cerevisiae* 균주에서 리보좀 발생 기능과 리보좀 결합에 관여하는 요인들이 크게 영향을 받았다는 것을 보여준다. 리보좀 기능 장애는 남성의 불임, 신경학적 결함 등과 같은 몇몇 중요한 질병과 관련이 있는 것으로 알려져 있다.

또한, 정상 범주에서 벗어나게 촉진된 KEGG pathways 는 *S. cerevisiae* 의 세포들이 바이러스 복제와 확산에 대한 일종의 길항 반응으로 추정되나 추가적인 연구가 필요하다. 따라서 제 4 장에서 확인된 Nitazoxanide 의 잠재적인 부작용은 향후 Nitazoxanide 가 항바이러스 제제로 사용되기 전 필수적으로 고려해야 하는 중요한 요인으로 여겨진다.

요약하면, 이 논문은 전사체 수준의 변화를 매우 효과적으로 탐지하는 기술인 RNA 시퀀싱을 사용하여 *S. cerevisiae* 에 대한 항바이러스 제제의 영향을 전사체 수준에서 기술하였고, 사람과 다른 진핵 생물에 대한 잠재적 부작용 및 그 영향에 관한 중요한 정보는 의약품 및 의료 산업에 큰 가치가 있다. 또한 환경 적 위험 평가를 위한 통찰력을 제공하여 항 바이러스제가 환경으로 방출 될 때 환경중의 다른 진핵 생물에도 유사한 결함이 발생할 수 있다. 게다가,이 연구는 중요한 항 바이러스 약품을 스크리닝하여 잠재적인 부작용을 찾는 새롭고 효율적인 방법을 제시하였다.

중심어: *S. cerevisiae*, ribavirin, nitazoxanide,항바이러스 제제, 부작용, mycovirus, RNA 시퀀싱

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